100839

SM

CASE

STIC-Biotech/ChemLib

From: Spector, Lorraine
Sent: Monday, August 11, 2003 1:39 PM
To: STIC-Biotech/ChemLib
Subject: SEARCH request for Serial No. 09/938418

STIC,

Please search SEQ ID NO: 2 (nucleic acid) and 7 (protein). For the protein, please ALSO do a word search with word size of 6 amino acids.
-pending
-issued
-commercial

Thanks.

Lorraine Spector
703-308-1793
U.S. Patent and Trademark Office
Art Unit 1647
lorraine.spector@uspto.gov
CM1-10B11
Mailbox 10-B19

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 8/13
Date Completed: 8/21
Searcher Prep/Review: SK
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 100839

TO: Lorraine Spector
Location: cm-1/10b19
Art Unit: 1647
Thursday, August 21, 2003
Case Serial Number: 09938418

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Spector,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:25:12 ; Search time 373 Seconds
(without alignments)
567.016 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	243	1	PCT-US02-02781-4559	Sequence 4559, Ap
2	1301	100.0	243	1	PCT-US02-12378-514	Sequence 514, App
3	1301	100.0	243	23	US-09-834-759-514	Sequence 514, App
4	1301	100.0	243	24	US-09-938-418-7	Sequence 7, Appli
5	1301	100.0	243	24	US-09-946-374-352	Sequence 352, App
6	1301	100.0	243	24	US-09-946-374-431	Sequence 431, App
7	1301	100.0	243	26	US-10-006-041A-352	Sequence 352, App
8	1301	100.0	243	26	US-10-006-041A-431	Sequence 431, App
9	1301	100.0	243	26	US-10-006-063A-352	Sequence 352, App
10	1301	100.0	243	26	US-10-006-063A-431	Sequence 431, App
11	1301	100.0	243	26	US-10-006-116A-352	Sequence 352, App
12	1301	100.0	243	26	US-10-006-116A-431	Sequence 431, App
13	1301	100.0	243	26	US-10-006-117A-352	Sequence 352, App
14	1301	100.0	243	26	US-10-006-117A-431	Sequence 431, App
15	1301	100.0	243	26	US-10-006-130A-352	Sequence 352, App
16	1301	100.0	243	26	US-10-006-130A-431	Sequence 431, App
17	1301	100.0	243	26	US-10-006-172A-352	Sequence 352, App
18	1301	100.0	243	26	US-10-006-172A-431	Sequence 431, App
19	1301	100.0	243	26	US-10-006-485A-352	Sequence 352, App
20	1301	100.0	243	26	US-10-006-485A-431	Sequence 431, App
21	1301	100.0	243	26	US-10-006-746A-352	Sequence 352, App
22	1301	100.0	243	26	US-10-006-746A-431	Sequence 431, App
23	1301	100.0	243	26	US-10-006-768A-352	Sequence 352, App
24	1301	100.0	243	26	US-10-006-768A-431	Sequence 431, App
25	1301	100.0	243	26	US-10-006-818A-352	Sequence 352, App
26	1301	100.0	243	26	US-10-006-818A-431	Sequence 431, App
27	1301	100.0	243	26	US-10-006-856A-352	Sequence 352, App
28	1301	100.0	243	26	US-10-006-856A-431	Sequence 431, App
29	1301	100.0	243	26	US-10-006-867-122	Sequence 122, App
30	1301	100.0	243	26	US-10-007-194A-352	Sequence 352, App
31	1301	100.0	243	26	US-10-007-194A-431	Sequence 431, App
32	1301	100.0	243	26	US-10-007-236A-352	Sequence 352, App
33	1301	100.0	243	26	US-10-007-236A-431	Sequence 431, App
34	1301	100.0	243	26	US-10-007-805-514	Sequence 514, App
35	1301	100.0	243	26	US-10-011-671A-352	Sequence 352, App
36	1301	100.0	243	26	US-10-011-671A-431	Sequence 431, App
37	1301	100.0	243	26	US-10-011-692A-352	Sequence 352, App
38	1301	100.0	243	26	US-10-011-692A-431	Sequence 431, App
39	1301	100.0	243	26	US-10-011-795A-352	Sequence 352, App
40	1301	100.0	243	26	US-10-011-795A-431	Sequence 431, App
41	1301	100.0	243	26	US-10-011-795B-352	Sequence 352, App
42	1301	100.0	243	26	US-10-011-795B-431	Sequence 431, App
43	1301	100.0	243	26	US-10-011-833A-352	Sequence 352, App
44	1301	100.0	243	26	US-10-011-833A-431	Sequence 431, App
45	1301	100.0	243	26	US-10-012-064A-352	Sequence 352, App

ALIGNMENTS

RESULT 1
PCT-US02-02781-4559
; Sequence 4559, Application PC/TUS0202781
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566PC
; CURRENT APPLICATION NUMBER: PCT/US02/02781
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4559
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-02781-4559

Query Match 100.0%; Score 1301; DB 1; Length 243;

```
  Best Local Similarity   100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 2
PCT-US02-12378-514
; Sequence 514, Application PC/TUS0212378
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.47003PC
;  CURRENT APPLICATION NUMBER: PCT/US02/12378
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-12378-514

  Query Match             100.0%;  Score 1301;  DB 1;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 3
US-09-834-759-514
; Sequence 514, Application US/09834759
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-514

  Query Match             100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 4
US-09-938-418-7
; Sequence 7, Application US/09938418
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Polakis,Paul
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Wu,Thomas D.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF TUMOR
;  FILE REFERENCE: P5009R1
;  CURRENT APPLICATION NUMBER: US/09/938,418
```

```
;  CURRENT FILING DATE:  2001-08-23
;  PRIOR APPLICATION NUMBER: 60/081,071
;  PRIOR FILING DATE: 1998-04-07
;  PRIOR APPLICATION NUMBER: 60/085,697
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/097,022
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/101,922
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/103,679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: PCT/US99/05028
;  PRIOR FILING DATE: 1999-03-08
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: PCT/US99/20111
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US00/04342
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-938-418-7

  Query Match           100.0%;  Score 1301;  DB 24;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243

RESULT 5
US-09-946-374-352
; Sequence 352, Application US/09946374
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
```

; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 1301; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 6
US-09-946-374-431
; Sequence 431, Application US/09946374
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
```

```
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27

  Query Match           100.0%;  Score 1301;  DB 24;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 7
US-10-006-041A-352
; Sequence 352, Application US/10006041A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C8
;  CURRENT APPLICATION NUMBER: US/10/006,041A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-041A-352

  Query Match           100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
```

```
Db        241 LPK 243


RESULT 8
US-10-006-041A-431
; Sequence 431, Application US/10006041A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C8
;  CURRENT APPLICATION NUMBER: US/10/006,041A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-041A-431

  Query Match            100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 9
US-10-006-063A-352
; Sequence 352, Application US/10006063A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C3
;  CURRENT APPLICATION NUMBER: US/10/006,063A
;  CURRENT FILING DATE:  2002-03-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-063A-352

  Query Match            100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 10
US-10-006-063A-431
; Sequence 431, Application US/10006063A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C3
;  CURRENT APPLICATION NUMBER: US/10/006,063A
;  CURRENT FILING DATE:  2002-03-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-063A-431
```

```
  Query Match           100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 11
US-10-006-116A-352
; Sequence 352, Application US/10006116A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
```

; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 1301; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-118;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 12
US-10-006-116A-431
; Sequence 431, Application US/10006116A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21

```
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match            100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 13
US-10-006-117A-352
; Sequence 352, Application US/10006117A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-117A-352

  Query Match            100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
US-10-006-117A-431
; Sequence 431, Application US/10006117A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-117A-431

  Query Match            100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
US-10-006-130A-352
; Sequence 352, Application US/10006130A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-130A-352

  Query Match             100.0%;  Score 1301;  DB 26;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-118;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


Search completed: August 13, 2003, 13:35:04
Job time : 375 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:25:42 ; Search time 22 Seconds
(without alignments)
241.089 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105250 seqs, 21826969 residues

Total number of hits satisfying chosen parameters: 105250

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1294	99.5	243	1	PCT-US02-29560A-203	Sequence 203, App
2	122.5	9.4	1737	7	US-60-487-610-1777	Sequence 1777, Ap
3	122.5	9.4	1737	7	US-60-485-450-1149	Sequence 1149, Ap
4	120	9.2	287	6	US-10-450-186-26	Sequence 26, Appl
5	118.5	9.1	614	7	US-60-487-610-2410	Sequence 2410, Ap
6	118.5	9.1	614	7	US-60-485-450-1524	Sequence 1524, Ap
7	118.5	9.1	1164	7	US-60-487-610-2411	Sequence 2411, Ap
8	118.5	9.1	1164	7	US-60-485-450-1525	Sequence 1525, Ap
9	118.5	9.1	1284	7	US-60-487-610-2407	Sequence 2407, Ap
10	118.5	9.1	1284	7	US-60-485-450-1521	Sequence 1521, Ap
11	118.5	9.1	1464	1	PCT-US02-18638A-36	Sequence 36, Appl
12	118.5	9.1	1464	6	US-10-291-265-243	Sequence 243, App
13	118.5	9.1	1464	7	US-60-487-610-2409	Sequence 2409, Ap
14	118.5	9.1	1464	7	US-60-485-450-1523	Sequence 1523, Ap
15	118	9.1	832	6	US-10-408-765A-1776	Sequence 1776, Ap
16	116	8.9	1110	7	US-60-487-610-2823	Sequence 2823, Ap
17	116	8.9	1180	7	US-60-487-610-2820	Sequence 2820, Ap
18	116	8.9	1184	7	US-60-487-610-2818	Sequence 2818, Ap
19	116	8.9	1184	7	US-60-487-610-2824	Sequence 2824, Ap
20	116	8.9	1283	7	US-60-487-610-2816	Sequence 2816, Ap
21	116	8.9	1381	7	US-60-487-610-2825	Sequence 2825, Ap
22	116	8.9	1406	7	US-60-487-610-2821	Sequence 2821, Ap
23	116	8.9	1480	7	US-60-487-610-2822	Sequence 2822, Ap
24	116	8.9	1579	7	US-60-487-610-2817	Sequence 2817, Ap
25	116	8.9	1677	7	US-60-487-610-2819	Sequence 2819, Ap
26	116	8.9	1685	7	US-60-487-610-2046	Sequence 2046, Ap
27	115.5	8.9	289	6	US-10-408-765A-1762	Sequence 1762, Ap
28	115.5	8.9	1336	7	US-60-487-610-1544	Sequence 1544, Ap
29	115.5	8.9	1336	7	US-60-485-450-993	Sequence 993, App
30	115.5	8.9	1516	7	US-60-487-610-1543	Sequence 1543, Ap
31	115.5	8.9	1516	7	US-60-485-450-992	Sequence 992, App
32	115.5	8.9	1669	6	US-10-286-897-5794	Sequence 5794, Ap
33	115.5	8.9	1672	6	US-10-286-897-2222	Sequence 2222, Ap
34	115	8.8	266	1	PCT-US03-21703-46	Sequence 46, Appl
35	115	8.8	286	1	PCT-US03-21703-44	Sequence 44, Appl
36	114.5	8.8	1356	7	US-60-487-610-1713	Sequence 1713, Ap
37	113.5	8.7	1268	7	US-60-487-610-2047	Sequence 2047, Ap
38	113.5	8.7	1283	7	US-60-487-610-2045	Sequence 2045, Ap
39	113.5	8.7	1669	7	US-60-487-610-1686	Sequence 1686, Ap
40	113	8.7	2629	7	US-60-487-610-2723	Sequence 2723, Ap
41	113	8.7	2944	7	US-60-490-890-372	Sequence 372, App
42	112	8.6	116	7	US-60-487-610-2153	Sequence 2153, Ap
43	112	8.6	245	6	US-10-286-897-1997	Sequence 1997, Ap
44	112	8.6	277	6	US-10-286-897-5569	Sequence 5569, Ap
45	112	8.6	392	1	PCT-US03-21703-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
PCT-US02-29560A-203
; Sequence 203, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-203

Query Match 99.5%; Score 1294; DB 1; Length 243;
Best Local Similarity 99.6%; Pred. No. 3.1e-124;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
```

```
Db        241 LPK 243


RESULT 2
US-60-487-610-1777
; Sequence 1777, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1777
;   LENGTH: 1737
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-1777

  Query Match             9.4%;  Score 122.5;  DB 7;  Length 1737;
  Best Local Similarity   35.0%;  Pred. No. 0.00057;
  Matches   35;  Conservative    8;  Mismatches   28;  Indels   29;  Gaps    4;

Qy         20 LLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGA---NVIPG 76
              :| |:|: ||:                        :||| | ||| |||||      ||
Db       1638 ILNQIPSHSSSIR--------------------TVQGPPGEPGRPGSPGAPGEQGPPG 1675

Qy         77 TPGIPGRDGFKGEKGE--CLRESF--EESWTPNYKQCSWS 112
              ||| ||  |  |  ||   |  :|  | :| |    ||:
Db       1676 TPGFPGNAGVPGTPGERGKLGPTFRGESAWQPWAPWLSWT 1715


RESULT 3
US-60-485-450-1149
; Sequence 1149, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1149
;   LENGTH: 1737
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1149

  Query Match             9.4%;  Score 122.5;  DB 7;  Length 1737;
  Best Local Similarity   35.0%;  Pred. No. 0.00057;
  Matches   35;  Conservative    8;  Mismatches   28;  Indels   29;  Gaps    4;

Qy         20 LLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGA---NVIPG 76
              :| |:|: ||:                        :||| | ||| |||||      ||
Db       1638 ILNQIPSHSSSIR--------------------TVQGPPGEPGRPGSPGAPGEQGPPG 1675

Qy         77 TPGIPGRDGFKGEKGE--CLRESF--EESWTPNYKQCSWS 112
              ||| ||  |  |  ||   |  :|  | :| |    ||:
Db       1676 TPGFPGNAGVPGTPGERGKLGPTFRGESAWQPWAPWLSWT 1715


RESULT 4
US-10-450-186-26
; Sequence 26, Application US/10450186
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION; GRIFFIN, Jennifer A.;
;  APPLICANT:  YAO, Monique G.; DUGGAN, Brendan M.;
;  APPLICANT:  YUE, Henry; DING, Li;
;  APPLICANT:  LAL, Preeti G.; LEE, Ernestine A.;
;  APPLICANT:  RAMKUMAR, Jayalaxmi; THANGAVELU, Kavitha;
;  APPLICANT:  XU, Yuming;    LEE, Sally;
;  APPLICANT:  TANG, Y. Tom; NGUYEN, Danniel B.;
;  APPLICANT:  WARREN, Bridget A.; HONCHELL, Cynthia D.;
;  APPLICANT:  GIETZEN, Kimberly J.; BAUGHN, Mariah R.;
;  APPLICANT:  GANDHI, Ameena R.; ARVIZU, Chandra S.;
;  APPLICANT:  CHAWLA, Narinder K.; LU, Yan;
;  APPLICANT:  ELLIOTT, Vicki S.; LU, Dyung Aina M.;
;  APPLICANT:  HAFALIA, April J.A.; AZIMZAI, Yalda;
;  APPLICANT:  KHAN, Farrah A.; TRAN, Uyen K.
;  TITLE OF INVENTION: SECRETED PROTEINS
;  FILE REFERENCE: PI-0345 USN
;  CURRENT APPLICATION NUMBER: US/10/450,186
;  CURRENT FILING DATE:  2003-06-09
;  PRIOR APPLICATION NUMBER: PCT/US01/48517
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,639
;  PRIOR FILING DATE: 2000-12-13
;  PRIOR APPLICATION NUMBER: US 60/257,852
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: US 60/260,105
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/262,932
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/263,096
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: US 60/263,090
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: US 60/265,926
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PERL Program
; SEQ ID NO 26
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7485334CD1
US-10-450-186-26

  Query Match             9.2%;  Score 120;  DB 6;  Length 287;
  Best Local Similarity   34.7%;  Pred. No. 0.0001;
  Matches   42;  Conservative   10;  Mismatches   57;  Indels   12;  Gaps    4;

Qy         27 PSSASEIPKGKQKAQLRQREVV-DLYNG---MCLQGPAGVPGRDGSPGANVIPGTPGIPG 82
              |: |   | |   | |   ||: ||        :||| | ||| | ||    || || ||
Db         44 PAGAKAPPPGPSTAAL---EVMQDLSANPPPPFIQGPKGDPGRPGKPGPRGPPGEPGPPG 100

Qy         83 RDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFS 142
                | ||||:  |       |  :  : ::   |:  |      |:    |||   ||
Db        101 PRGPPGEKGDSGRPGL-----PGLQLTTSAAGGVGVVSGGTGGGGDTEGEVTSALSAAFS 155

Qy        143 G 143
              |
Db        156 G 156


RESULT 5
US-60-487-610-2410
; Sequence 2410, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
```

```
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2410
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2410

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 614;
  Best Local Similarity   36.3%;  Pred. No. 0.00038;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                     |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 6
US-60-485-450-1524
; Sequence 1524, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1524
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1524

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 614;
  Best Local Similarity   36.3%;  Pred. No. 0.00038;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                     |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 7
US-60-487-610-2411
; Sequence 2411, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2411
;   LENGTH: 1164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2411

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1164;
  Best Local Similarity   36.3%;  Pred. No. 0.00087;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                     |||
Db         57 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 85

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db         86 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 116


RESULT 8
US-60-485-450-1525
; Sequence 1525, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1525
;   LENGTH: 1164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1525

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1164;
  Best Local Similarity   36.3%;  Pred. No. 0.00087;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                     |||
Db         57 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 85

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db         86 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 116


RESULT 9
US-60-487-610-2407
; Sequence 2407, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2407
;   LENGTH: 1284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2407

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1284;
  Best Local Similarity   36.3%;  Pred. No. 0.00099;
```

```
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                      |||
Db        177 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 205

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        206 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 236


RESULT 10
US-60-485-450-1521
; Sequence 1521, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1521
;   LENGTH: 1284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1521

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1284;
  Best Local Similarity   36.3%;  Pred. No. 0.00099;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                      |||
Db        177 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 205

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        206 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 236


RESULT 11
PCT-US02-18638A-36
; Sequence 36, Application PC/TUS0218638A
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc. et al.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035PC
;  CURRENT APPLICATION NUMBER: PCT/US02/18638A
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-18638A-36

  Query Match             9.1%;  Score 118.5;  DB 1;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.0012;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                      |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 12
US-10-291-265-243
; Sequence 243, Application US/10291265
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-243

  Query Match             9.1%;  Score 118.5;  DB 6;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.0012;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                      |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 13
US-60-487-610-2409
; Sequence 2409, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2409
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2409

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.0012;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;
```

```
Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 14
US-60-485-450-1523
; Sequence 1523, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1523
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1523

  Query Match             9.1%;  Score 118.5;  DB 7;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.0012;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 15
US-10-408-765A-1776
; Sequence 1776, Application US/10408765A
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1776
;   LENGTH: 832
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-1776

  Query Match             9.1%;  Score 118;  DB 6;  Length 832;
  Best Local Similarity   47.8%;  Pred. No. 0.00063;
  Matches   33;  Conservative    4;  Mismatches   26;  Indels    6;  Gaps    3;

Qy         25 PAPSSASEIPKGKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIPGTPGIPGR 83
              |  |  :| ||||| ||    |  |    |  | || |·| || |  |   | |  |:|||

Db        367 PKGSKGAEGPKGKQGKAGAPGRRGVQGLQG--LPGPRGVVGRQGLEG---IAGPDGLPGR 421

Qy         84 DGFKGEKGE 92
              ||  |::||
Db        422 DGQAGQQGE 430


Search completed: August 13, 2003, 13:35:32
Job time : 23 secs.
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:27:27 ; Search time 55 Seconds
(without alignments)
578.796 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	243	10	US-09-938-418-7	Sequence 7, Appli
2	1301	100.0	243	11	US-09-946-374-352	Sequence 352, App
3	1301	100.0	243	11	US-09-946-374-431	Sequence 431, App
4	1301	100.0	243	12	US-10-015-387A-352	Sequence 352, App
5	1301	100.0	243	12	US-10-015-387A-431	Sequence 431, App
6	1301	100.0	243	12	US-10-063-735-122	Sequence 122, App
7	1301	100.0	243	12	US-10-006-130A-352	Sequence 352, App
8	1301	100.0	243	12	US-10-006-130A-431	Sequence 431, App
9	1301	100.0	243	12	US-10-199-672-366	Sequence 366, App
10	1301	100.0	243	14	US-10-006-867-122	Sequence 122, App
11	1301	100.0	243	14	US-10-052-586-366	Sequence 366, App
12	1301	100.0	243	14	US-10-007-805-514	Sequence 514, App
13	1301	100.0	243	14	US-10-063-547-122	Sequence 122, App
14	1301	100.0	243	15	US-10-174-590-366	Sequence 366, App
15	1301	100.0	243	15	US-10-176-758-366	Sequence 366, App
16	1301	100.0	243	15	US-10-175-737-366	Sequence 366, App
17	1301	100.0	243	15	US-10-063-616-122	Sequence 122, App
18	1301	100.0	243	15	US-10-173-706-366	Sequence 366, App
19	1301	100.0	243	15	US-10-175-738-366	Sequence 366, App
20	1301	100.0	243	15	US-10-175-752-366	Sequence 366, App
21	1301	100.0	243	15	US-10-176-482-366	Sequence 366, App
22	1301	100.0	243	15	US-10-176-757-366	Sequence 366, App
23	1301	100.0	243	15	US-10-176-913-366	Sequence 366, App
24	1301	100.0	243	15	US-10-180-552-366	Sequence 366, App
25	1301	100.0	243	15	US-10-180-557-366	Sequence 366, App
26	1301	100.0	243	15	US-10-076-622-514	Sequence 514, App
27	1301	100.0	243	15	US-10-063-502-122	Sequence 122, App
28	1301	100.0	243	15	US-10-173-700-366	Sequence 366, App
29	1301	100.0	243	15	US-10-174-572-366	Sequence 366, App
30	1301	100.0	243	15	US-10-174-579-366	Sequence 366, App
31	1301	100.0	243	15	US-10-174-582-366	Sequence 366, App
32	1301	100.0	243	15	US-10-174-588-366	Sequence 366, App
33	1301	100.0	243	15	US-10-175-739-366	Sequence 366, App
34	1301	100.0	243	15	US-10-175-740-366	Sequence 366, App
35	1301	100.0	243	15	US-10-175-743-366	Sequence 366, App
36	1301	100.0	243	15	US-10-176-488-366	Sequence 366, App
37	1301	100.0	243	15	US-10-176-492-366	Sequence 366, App
38	1301	100.0	243	15	US-10-176-747-366	Sequence 366, App
39	1301	100.0	243	15	US-10-176-750-366	Sequence 366, App
40	1301	100.0	243	15	US-10-176-985-366	Sequence 366, App
41	1301	100.0	243	15	US-10-176-987-366	Sequence 366, App
42	1301	100.0	243	15	US-10-176-992-366	Sequence 366, App
43	1301	100.0	243	15	US-10-176-993-366	Sequence 366, App
44	1301	100.0	243	15	US-10-184-658-366	Sequence 366, App
45	1301	100.0	243	15	US-10-176-991-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-09-938-418-7
; Sequence 7, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Gurney,Austin L.
; APPLICANT: Polakis,Paul
; APPLICANT: Williams,P.Mickey
; APPLICANT: Wood,William I.
; APPLICANT: Wu,Thomas D.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342

```
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-938-418-7

  Query Match             100.0%;  Score 1301;  DB 10;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 2
US-09-946-374-352
; Sequence 352, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
```

; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1301; DB 11; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.7e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 3
US-09-946-374-431
; Sequence 431, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01

```
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match           100.0%;  Score 1301;  DB 11;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 4
US-10-015-387A-352
; Sequence 352, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C54
;  CURRENT APPLICATION NUMBER: US/10/015,387A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-015-387A-352

  Query Match           100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 5
US-10-015-387A-431
; Sequence 431, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
```

```
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C54
;  CURRENT APPLICATION NUMBER: US/10/015,387A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-015-387A-431

  Query Match            100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 6
US-10-063-735-122
; Sequence 122, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,735
;  CURRENT FILING DATE:  2002-05-08
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-735-122

  Query Match            100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 7
US-10-006-130A-352
; Sequence 352, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-130A-352

  Query Match            100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
```

```
                |||
Db        241 LPK 243


RESULT 8
US-10-006-130A-431
; Sequence 431, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-130A-431

  Query Match             100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 9
US-10-199-672-366
; Sequence 366, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/199,672
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-199-672-366

  Query Match             100.0%;  Score 1301;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 10
US-10-006-867-122
; Sequence 122, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/096012
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096757
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096949
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/096959
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/097954
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097971
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097979
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23

```
;  PRIOR APPLICATION NUMBER: 60/114223
;  PRIOR FILING DATE: 1998-12-30
;  PRIOR APPLICATION NUMBER: 60/115614
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116527
;  PRIOR FILING DATE: 1999-01-20
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/119285
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: 60/119287
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: 60/119525
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/119549
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/120014
;  PRIOR FILING DATE: 1999-02-11
;  PRIOR APPLICATION NUMBER: 60/129122
;  PRIOR FILING DATE: 1999-04-13
;  PRIOR APPLICATION NUMBER: 60/129674
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/131291
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/138387
;  PRIOR FILING DATE: 1999-06-09
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/169495
;  PRIOR FILING DATE: 1999-12-07
;  PRIOR APPLICATION NUMBER: 60/175481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 60/191007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/199397
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/380139
;  PRIOR FILING DATE: 1998-08-25
;  PRIOR APPLICATION NUMBER: 09/311832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 09/380137
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/380138
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/380142

  Query Match           100.0%;  Score 1301;  DB 14;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 11
US-10-052-586-366
;  Sequence 366, Application US/10052586
;  Publication No. US20020127584A1
;  GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT:  Chen,Jian
;   APPLICANT:  Desnoyers,Luc
;   APPLICANT:  Goddard,Audrey
;   APPLICANT:  Godowski,Paul J.
;   APPLICANT:  Gurney,Austin L.
;   APPLICANT:  Pan,James
;   APPLICANT:  Smith,Victoria
;   APPLICANT:  Watanabe,Colin K.
;   APPLICANT:  Wood,William I.
;   APPLICANT:  Zhang,Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3430R1C1
;   CURRENT APPLICATION NUMBER: US/10/052,586
;   CURRENT FILING DATE:  2002-01-15
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/059266
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/063120
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063121
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063486
;   PRIOR FILING DATE: 1997-10-21
;   PRIOR APPLICATION NUMBER: 60/063540
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063541
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063544
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063564
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063734
;   PRIOR FILING DATE: 1997-10-29
;   PRIOR APPLICATION NUMBER: 60/063870
;   PRIOR FILING DATE: 1997-10-31
;   PRIOR APPLICATION NUMBER: 60/064103
;   PRIOR FILING DATE: 1997-10-31
;   PRIOR APPLICATION NUMBER: 60/065311
;   PRIOR FILING DATE: 1997-11-13
;   PRIOR APPLICATION NUMBER: 60/066120
;   PRIOR FILING DATE: 1997-11-21
;   PRIOR APPLICATION NUMBER: 60/066466
;   PRIOR FILING DATE: 1997-11-24
;   PRIOR APPLICATION NUMBER: 60/066772
;   PRIOR FILING DATE: 1997-11-24
;   PRIOR APPLICATION NUMBER: 60/069335
;   PRIOR FILING DATE: 1997-12-11
;   PRIOR APPLICATION NUMBER: 60/069425
;   PRIOR FILING DATE: 1997-12-12
;   PRIOR APPLICATION NUMBER: 60/069870
;   PRIOR FILING DATE: 1997-12-17
;   PRIOR APPLICATION NUMBER: 60/068017
;   PRIOR FILING DATE: 1997-12-18
;   PRIOR APPLICATION NUMBER: 60/077450
;   PRIOR FILING DATE: 1998-03-10
;   PRIOR APPLICATION NUMBER: 60/077632
;   PRIOR FILING DATE: 1998-03-11
;   PRIOR APPLICATION NUMBER: 60/077649
;   PRIOR FILING DATE: 1998-03-11
;   PRIOR APPLICATION NUMBER: 60/078886
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR APPLICATION NUMBER: 60/078939
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR APPLICATION NUMBER: 60/079664
;   PRIOR FILING DATE: 1998-03-27
```

; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1301; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.7e-121;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 12
US-10-007-805-514
; Sequence 514, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C10
;  CURRENT APPLICATION NUMBER: US/10/007,805
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-805-514

  Query Match           100.0%;  Score 1301;  DB 14;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 13
US-10-063-547-122
; Sequence 122, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,547
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-547-122

  Query Match           100.0%;  Score 1301;  DB 14;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
US-10-174-590-366
; Sequence 366, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-174-590-366

  Query Match           100.0%;  Score 1301;  DB 15;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
US-10-176-758-366
; Sequence 366, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-758-366

  Query Match            100.0%;  Score 1301;  DB 15;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-121;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

Search completed: August 13, 2003, 13:36:36
Job time : 57 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:23:42 ; Search time 29 Seconds
(without alignments)
354.536 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1291	99.2	243	4	US-09-489-847-205	Sequence 205, App
2	1100.5	84.6	276	4	US-09-205-258-958	Sequence 958, App
3	356	27.4	66	4	US-09-205-258-962	Sequence 962, App
4	296	22.8	52	4	US-09-205-258-961	Sequence 961, App
5	270	20.8	51	4	US-09-205-258-963	Sequence 963, App
6	211.5	16.3	52	4	US-09-205-258-960	Sequence 960, App
7	196	15.1	93	4	US-09-489-847-240	Sequence 240, App
8	196	15.1	93	4	US-09-489-847-362	Sequence 362, App
9	122.5	9.4	246	2	US-08-463-911-4	Sequence 4, Appli
10	118.5	9.1	1057	3	US-08-931-820-1	Sequence 1, Appli
11	118.5	9.1	1461	4	US-09-585-887-9	Sequence 9, Appli
12	118.5	9.1	1461	4	US-09-289-578-9	Sequence 9, Appli
13	115.5	8.9	128	4	US-09-227-357-190	Sequence 190, App
14	115	8.8	623	3	US-09-029-348-3	Sequence 3, Appli
15	115	8.8	626	3	US-09-029-348-2	Sequence 2, Appli
16	113.5	8.7	1694	1	US-08-494-168-2	Sequence 2, Appli
17	111	8.5	245	4	US-09-552-225A-4	Sequence 4, Appli
18	110.5	8.5	310	3	US-09-219-849-47	Sequence 47, Appl
19	110.5	8.5	595	3	US-09-219-849-48	Sequence 48, Appl
20	110.5	8.5	595	3	US-09-219-849-50	Sequence 50, Appl
21	110.5	8.5	684	1	US-08-555-669-12	Sequence 12, Appl
22	110.5	8.5	684	3	US-09-073-663-12	Sequence 12, Appl
23	110.5	8.5	822	3	US-09-219-849-49	Sequence 49, Appl
24	110	8.5	1568	3	US-09-181-706-2	Sequence 2, Appli
25	110	8.5	1568	3	US-09-458-791-2	Sequence 2, Appli
26	110	8.5	1568	3	US-09-459-066-2	Sequence 2, Appli
27	110	8.5	1568	4	US-09-459-065-2	Sequence 2, Appli
28	108.5	8.3	1060	3	US-08-931-820-3	Sequence 3, Appli
29	108.5	8.3	1418	3	US-08-963-825-20	Sequence 20, Appl
30	108.5	8.3	1418	3	US-09-010-999-1	Sequence 1, Appli
31	108.5	8.3	1418	4	US-09-500-811-20	Sequence 20, Appl
32	108.5	8.3	1418	4	US-09-570-573-20	Sequence 20, Appl
33	108.5	8.3	1418	4	US-09-548-608-20	Sequence 20, Appl
34	108.5	8.3	1442	2	US-08-316-650-12	Sequence 12, Appl
35	108.5	8.3	1442	5	PCT-US95-02251-12	Sequence 12, Appl
36	108	8.3	1057	3	US-08-931-820-4	Sequence 4, Appli
37	108	8.3	1078	3	US-08-963-825-21	Sequence 21, Appl
38	108	8.3	1078	4	US-09-500-811-21	Sequence 21, Appl
39	108	8.3	1078	4	US-09-570-573-21	Sequence 21, Appl
40	108	8.3	1078	4	US-09-548-608-21	Sequence 21, Appl
41	106.5	8.2	349	6	5510466-2	Patent No. 5510466
42	106.5	8.2	453	6	5510466-4	Patent No. 5510466
43	106.5	8.2	546	1	US-08-494-168-10	Sequence 10, Appl
44	106.5	8.2	1341	3	US-08-963-825-18	Sequence 18, Appl
45	106.5	8.2	1341	4	US-09-500-811-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-489-847-205
; Sequence 205, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-205

Query Match 99.2%; Score 1291; DB 4; Length 243;
Best Local Similarity 99.2%; Pred. No. 4e-127;
Matches 241; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCERWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
```

```
Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 2
US-09-205-258-958
; Sequence 958, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 958
;   LENGTH: 276
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (10)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-958

  Query Match             84.6%;  Score 1100.5;  DB 4;  Length 276;
  Best Local Similarity   96.7%;  Pred. No. 4.2e-107;
  Matches  203;  Conservative    3;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         34 PKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGEC 93
              |:|  | ::|||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         68 PRG-SKRRIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGEC 126

Qy         94 LRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNAC 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 LRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNAC 186

Qy        154 CQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAI 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAI 246

Qy        214 WVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
              ||||||||||||||||||||||||||||||
Db        247 WVGTCSDYPKGDASTGWNSVSRIIIEELPK 276


RESULT 3
US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
```

; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 962
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-962

Query Match 27.4%; Score 356; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.8e-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        128 FTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNS 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNS 60

Qy        188 TINIHR 193
              ||||||
Db         61 TINIHR 66
```

RESULT 4
US-09-205-258-961
; Sequence 961, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 961
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-961

Query Match 22.8%; Score 296; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.5e-24;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 TPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTF 128
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTF 52

RESULT 5
US-09-205-258-963
; Sequence 963, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 963
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-963

Query Match 20.8%; Score 270; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 RTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 RTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 51

RESULT 6
US-09-205-258-960
; Sequence 960, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-960

Query Match 16.3%; Score 211.5; DB 4; Length 52;
Best Local Similarity 85.1%; Pred. No. 4.6e-15;
Matches 40; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 34 PKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIPGTPGI 80
|:| | ::|||||||||||||||||||||||||||||| |||||||
Db 7 PRG-SKRRIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGI 52

RESULT 7
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 240
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-240

  Query Match             15.1%;  Score 196;  DB 4;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-13;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40
              ||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40


RESULT 8
US-09-489-847-362
; Sequence 362, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 362
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-362

  Query Match             15.1%;  Score 196;  DB 4;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-13;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40
              ||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40


RESULT 9
US-08-463-911-4
; Sequence 4, Application US/08463911
; Patent No. 5869330
;  GENERAL INFORMATION:
;    APPLICANT:  Scherer, Philipp E.
;    APPLICANT:  Lodish, Harvey F.
;    TITLE OF INVENTION:  A NOVEL SERUM PROTEIN PRODUCED
;    TITLE OF INVENTION:  EXCLUSIVELY IN ADIPOCYTES
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,911
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-463-911-4

  Query Match              9.4%;  Score 122.5;  DB 2;  Length 246;
  Best Local Similarity   37.4%;  Pred. No. 8.3e-05;
  Matches   34;  Conservative    5;  Mismatches   33;  Indels   19;  Gaps    2;

Qy          5 GPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
              ||:  ||    |||| || ||  | ||                |    : |  | ||
Db          4 GPSCQPQCGLCLLLLFLLALPLRSQAS---------------AGCYGIPGMPGMPGAPG 47

Qy         65 RDGS---PGANVIPGTPGIPGRDGFKGEKGE 92
              :||     |    || | :||  | ||:|||
Db         48 KDGHDGLQGPKGEPGIPAVPGTQGPKGQKGE 78


RESULT 10
US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Assay for collagen degradation
;    NUMBER OF SEQUENCES:  4
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/931,820
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 96202596.1
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1057 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Collagen type I
US-08-931-820-1

  Query Match              9.1%;  Score 118.5;  DB 3;  Length 1057;
  Best Local Similarity   36.3%;  Pred. No. 0.0017;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;
```

```
Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        196 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 224

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        225 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 255


RESULT 11
US-09-585-887-9
; Sequence 9, Application US/09585887
; Patent No. 6413742
; GENERAL INFORMATION:
;  APPLICANT: Olsen, David R
;  APPLICANT:  Chang, Robert
;  APPLICANT:  McMullin, Hugh
;  APPLICANT:  Hitzeman, Ronald A.
;  APPLICANT:  Chisholm, George
;  TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
;  TITLE OF INVENTION:  FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 225002030400
;  CURRENT APPLICATION NUMBER: US/09/585,887
;  CURRENT FILING DATE:  2000-05-31
;  PRIOR APPLICATION NUMBER: 09/289,578
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 60/084,828
;  PRIOR FILING DATE: 1998-05-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1461
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-585-887-9

  Query Match             9.1%;  Score 118.5;  DB 4;  Length 1461;
  Best Local Similarity   36.3%;  Pred. No. 0.0026;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        354 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 382

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        383 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 413


RESULT 12
US-09-289-578-9
; Sequence 9, Application US/09289578
; Patent No. 6428978
; GENERAL INFORMATION:
;  APPLICANT: Olsen, David R
;  APPLICANT:  Chang, Robert
;  APPLICANT:  McMullin, Hugh
;  APPLICANT:  Hitzeman, Ronald A.
;  APPLICANT:  Chisholm, George
;  TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
;  TITLE OF INVENTION:  FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 225002030400
;  CURRENT APPLICATION NUMBER: US/09/289,578
;  CURRENT FILING DATE:  1999-04-10
;  PRIOR APPLICATION NUMBER: 60/084,828
;  PRIOR FILING DATE: 1998-05-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 1461
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-289-578-9

  Query Match             9.1%;  Score 118.5;  DB 4;  Length 1461;
  Best Local Similarity   36.3%;  Pred. No. 0.0026;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        354 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 382

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        383 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 413


RESULT 13
US-09-227-357-190
; Sequence 190, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
```

```
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,954
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/058,785
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,664
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,660
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,661
;  EARLIER FILING DATE: 1997-09-12
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 190
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (127)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (128)
;   OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-190

  Query Match             8.9%;  Score 115.5;  DB 4;  Length 128;
  Best Local Similarity   46.3%;  Pred. No. 0.00018;
  Matches   31;  Conservative    5;  Mismatches   22;  Indels    9;  Gaps    3;

Qy         30 ASEIPKGKQKAQLRQREVVDLYNGMC----LQGPAGVPGRDGSPGANVIPGTPGIPGRDG 85
              ||  |:|    ||:       |  :|    | || | || :|||| :   | ||  ||||
Db         14 ASGQPRGN---QLKGENYSPRY--ICSIPGLPGPPGPPGANGSPGPHGRIGLPGRDGRDG 68

Qy         86 FKGEKGE 92
              |||||
Db         69 RKGEKGE 75


RESULT 14
US-09-029-348-3
; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
;  APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
;  TITLE OF INVENTION: NOVEL PROCOLLAGENS
;  FILE REFERENCE: d087857PUS LISTING
;  CURRENT APPLICATION NUMBER: US/09/029,348
;  CURRENT FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 623
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
;   OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
US-09-029-348-3

  Query Match             8.8%;  Score 115;  DB 3;  Length 623;
  Best Local Similarity   36.1%;  Pred. No. 0.0019;
  Matches   39;  Conservative    8;  Mismatches   47;  Indels   14;  Gaps    5;

Qy         22 LQLPAPSSASEIPKGKQKAQLRQREVVDLY--NGMCLQGPAGVPGRDGSPGANVIPGTPG 79
              |  | |    ||| |:  |   |          ||   ||| | ||  | || |  || ||
Db         72 LDCPNP----EIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPG 127

Qy         80 IPGRDGFKGEKGECLRESF---EESWTPNYKQCSWSSLNYGIDLGKIA 124
              ||  |  |  | |  ||     ::::| |       |   |: :| :|
Db        128 QPGSPGSPGPPGIC--ESCPTGPQNYSPQYDSYDVKS---GVAVGGLA 170


RESULT 15
US-09-029-348-2
; Sequence 2, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
;  APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
;  TITLE OF INVENTION: NOVEL PROCOLLAGENS
;  FILE REFERENCE: d087857PUS LISTING
;  CURRENT APPLICATION NUMBER: US/09/029,348
;  CURRENT FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 626
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
;   OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
US-09-029-348-2

  Query Match             8.8%;  Score 115;  DB 3;  Length 626;
  Best Local Similarity   36.1%;  Pred. No. 0.0019;
  Matches   39;  Conservative    8;  Mismatches   47;  Indels   14;  Gaps    5;

Qy         22 LQLPAPSSASEIPKGKQKAQLRQREVVDLY--NGMCLQGPAGVPGRDGSPGANVIPGTPG 79
              |  | |    ||| |:  |   |          ||   ||| | ||  | || |  || ||
Db         72 LDCPNP----EIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPG 127

Qy         80 IPGRDGFKGEKGECLRESF---EESWTPNYKQCSWSSLNYGIDLGKIA 124
              ||  |  |  | |  ||     ::::| |       |   |: :| :|
Db        128 QPGSPGSPGPPGIC--ESCPTGPQNYSPQYDSYDVKS---GVAVGGLA 170


Search completed: August 13, 2003, 13:28:42
Job time : 30 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:22:12 ; Search time 96 Seconds
(without alignments)
653.196 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1294	99.5	243	4	Q96CG8	Q96cg8 homo sapien
2	1216	93.5	245	11	Q8CG08	Q8cg08 rattus norv
3	1201	92.3	245	11	Q9D1D6	Q9d1d6 mus musculu
4	1052	80.9	232	4	Q8IX63	Q8ix63 homo sapien
5	132	10.1	565	11	Q8K036	Q8k036 mus musculu
6	124.5	9.6	717	4	Q9NQ52	Q9nq52 homo sapien
7	122.5	9.4	1472	13	Q90ZA0	Q90za0 gallus gall
8	120	9.2	287	11	Q8CFR0	Q8cfr0 mus musculu
9	120	9.2	1752	5	Q07265	Q07265 strongyloce
10	119	9.1	289	5	Q18799	Q18799 caenorhabdi
11	118.5	9.1	1461	4	O76045	O76045 homo sapien
12	118.5	9.1	1464	4	Q8N473	Q8n473 homo sapien
13	118	9.1	291	5	Q9NAR3	Q9nar3 caenorhabdi
14	118	9.1	832	4	Q96JF7	Q96jf7 homo sapien
15	118	9.1	1860	4	Q8IZC6	Q8izc6 homo sapien
16	117.5	9.0	568	11	Q8CD80	Q8cd80 mus musculu
17	117.5	9.0	739	11	O70575	O70575 mus musculu
18	117.5	9.0	751	11	Q9R1N9	Q9r1n9 mus musculu
19	117	9.0	327	5	O01799	O01799 caenorhabdi
20	117	9.0	1669	11	Q9QZS0	Q9qzs0 mus musculu
21	116	8.9	886	4	Q9NUB7	Q9nub7 homo sapien
22	116	8.9	888	13	Q90796	Q90796 gallus gall
23	115.5	8.9	1621	4	Q9H4R9	Q9h4r9 homo sapien
24	115.5	8.9	1684	6	Q8HYC1	Q8hyc1 canis famil
25	115	8.8	957	4	Q9H0V3	Q9h0v3 homo sapien
26	115	8.8	957	4	Q96P44	Q96p44 homo sapien
27	115	8.8	1163	4	Q8N6U4	Q8n6u4 homo sapien
28	114.5	8.8	311	5	O01904	O01904 caenorhabdi
29	114.5	8.8	496	4	Q8NE08	Q8ne08 homo sapien
30	114	8.8	304	5	Q9XVG3	Q9xvg3 caenorhabdi
31	114	8.8	304	5	Q9U349	Q9u349 caenorhabdi
32	114	8.8	304	5	Q9U348	Q9u348 caenorhabdi
33	114	8.8	312	11	Q8CHX9	Q8chx9 mus musculu
34	113.5	8.7	289	11	Q8BVD7	Q8bvd7 mus musculu
35	113.5	8.7	300	5	Q22183	Q22183 caenorhabdi
36	113.5	8.7	345	5	Q95WV2	Q95wv2 meloidogyne
37	113.5	8.7	1420	13	Q90W37	Q90w37 gallus gall
38	113.5	8.7	1549	11	Q60444	Q60444 cricetulus
39	113.5	8.7	1600	4	Q9UEH6	Q9ueh6 homo sapien
40	113.5	8.7	2944	11	Q63870	Q63870 mus musculu
41	112.5	8.6	1307	13	Q8JFF7	Q8jff7 xenopus lae
42	112	8.6	325	5	Q17402	Q17402 caenorhabdi
43	112	8.6	347	6	Q9XT25	Q9xt25 bos taurus
44	111.5	8.6	428	5	Q22369	Q22369 caenorhabdi
45	111.5	8.6	438	11	Q8K4P3	Q8k4p3 mus musculu

ALIGNMENTS

RESULT 1
Q96CG8
ID Q96CG8 PRELIMINARY; PRT; 243 AA.
AC Q96CG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 1110014B07 gene (Collagen triple helix
DE repeat-containing protein 1).
GN CTHRC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic smooth muscle;
RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RT "Expression of the novel collagen triple helix repeat-containing gene
RT (Cthrc1) suggests functions in multiple organ systems.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014245; AAH14245.1; -.
DR EMBL; AY136825; AAN15749.1; -.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF01391; Collagen; 1.
SQ SEQUENCE 243 AA; 26224 MW; A11FFEB1C66867F9 CRC64;

Query Match 99.5%; Score 1294; DB 4; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.7e-119;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

```
Qy          61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy         121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy         181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy         241 LPK 243
               |||
Db         241 LPK 243


RESULT 2
Q8CG08
ID   Q8CG08      PRELIMINARY;      PRT;   245 AA.
AC   Q8CG08;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Collagen triple helix repeat-containing protein 1.
GN   CTHRC1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RT   "Expression of the novel collagen triple helix repeat-containing gene
RT   (Cthrc1) suggests functions in multiple organ systems.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY136824; AAN15748.1; -.
SQ   SEQUENCE   245 AA;  26424 MW;  2296FD6DCDBA21F2 CRC64;

  Query Match             93.5%;  Score 1216;  DB 11;  Length 245;
  Best Local Similarity   94.3%;  Pred. No. 2.2e-111;
  Matches  231;  Conservative    3;  Mismatches    9;  Indels    2;  Gaps    1;

Qy          1 MRPQGPAASPQRLRG--LLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQG 58
              | ||| ||||| | |  |:||||||| ||||||| || |||| :|||||||||||||||
Db          1 MHPQGRAASPQLLLGLFLVLLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQG 60

Qy         59 PAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGI 118
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGI 120

Qy        119 DLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYL 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYL 180

Qy        179 DQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIII 238
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQGSPELNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIII 240

Qy        239 EELPK 243
              |||||
Db        241 EELPK 245


RESULT 3
Q9D1D6
ID   Q9D1D6      PRELIMINARY;      PRT;   245 AA.
AC   Q9D1D6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   1110014B07Rik protein.
GN   CTHRC1 OR 1110014B07RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003674; BAB22930.1; -.
DR   MGD; MGI:1915838; Cthrc1.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 1.
SQ   SEQUENCE   245 AA;  26460 MW;  14951B87D8181A0E CRC64;

  Query Match             92.3%;  Score 1201;  DB 11;  Length 245;
  Best Local Similarity   93.1%;  Pred. No. 6.6e-110;
  Matches  228;  Conservative    4;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 MRPQGPAASPQRLRG--LLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQG 58
              | ||| || || | |  |:||||||| || |||| || ||:| :|||||||||||||||
Db          1 MHPQGRAAPPQLLLGLFLVLLLLLQLSAPISASENPKVKQQALIRQREVVDLYNGMCLQG 60

Qy         59 PAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGI 118
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGI 120

Qy        119 DLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYL 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYL 180

Qy        179 DQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIII 238
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQGSPELNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIII 240

Qy        239 EELPK 243
              |||||
Db        241 EELPK 245


RESULT 4
Q8IX63
ID   Q8IX63      PRELIMINARY;      PRT;   232 AA.
AC   Q8IX63;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   NTMC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sanuki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
RT   "Novel polypeptide found in human cornea cDNA library.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF395488; AAO17919.1; -.
SQ   SEQUENCE   232 AA;  25163 MW;  E9D4BC30304837ED CRC64;

  Query Match            80.9%;  Score 1052;  DB 4;  Length 232;
  Best Local Similarity  83.1%;  Pred. No. 2.7e-95;
  Matches  201;  Conservative    8;  Mismatches   19;  Indels   14;  Gaps    2;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              | | | : :  :||   :   |:: ||:   :  ||           ||||||||||
Db          1 MWPPGRSIT-VKLREKTVSRKLEMNGPSAFQGLICGK------------YNGMCLQGPA 46

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         47 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 106

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 166

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 226

Qy        241 LP 242
              ||
Db        227 LP 228


RESULT 5
Q8K036
ID   Q8K036      PRELIMINARY;      PRT;   565 AA.
AC   Q8K036;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to collagen, type XIII, alpha 1.
GN   COL13A1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034164; AAH34164.1; -.
DR   MGD; MGI:1277201; Col13a1.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 5.
DR   ProDom; PD000007; Collagen; 1.
KW   Collagen.
SQ   SEQUENCE   565 AA;  56726 MW;  DBD3FF99D670195F CRC64;

  Query Match            10.1%;  Score 132;  DB 11;  Length 565;
  Best Local Similarity  33.9%;  Pred. No. 0.00024;
  Matches   38;  Conservative   13;  Mismatches   35;  Indels   26;  Gaps    6;

Qy         27 PSSASEI----PKGKQKAQLRQREVVDLYNG----------MCLQGPAGVPGRDGSPGA 71
              | :| |     |||  | :  : |:|| |||          : | || |:||: | ||
Db        393 PGAAGEQGPSGPKG-AKGEPGKGEMVD-YNGSINEALQEIRTLALMGPPGLPGQTGPPGP 450

Qy         72 NVIPGTP------GIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYG 117
                ||||      |:||  |  |:||   :      |:    :  |:| | |
Db        451 ---PGTPGQRGEIGLPGPPGHDGDKGPRGKPGDGAGWSSRTPRKGWASRNEG 499


RESULT 6
Q9NQ52
ID   Q9NQ52      PRELIMINARY;      PRT;   717 AA.
AC   Q9NQ52;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Type XIII collagen.
GN   COLXIIIA1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Snellman A., Tu H., Vaeisaenen T., Kvist A.P., Huhtala P.,
RA   Pihlajaniemi T.;
RT   "A short sequence in the N-terminal region is required for the
RT   trimerization of type XIII collagen and is conserved in other
RT   collagenous transmembrane proteins.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ293624; CAC00688.1; -.
DR   Genew; HGNC:2190; COL13A1.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 9.
DR   ProDom; PD000007; Collagen; 1.
KW   Collagen.
SQ   SEQUENCE   717 AA;  69964 MW;  A311E9C7D3E87577 CRC64;

  Query Match             9.6%;  Score 124.5;  DB 4;  Length 717;
  Best Local Similarity   42.1%;  Pred. No. 0.0018;
  Matches   32;  Conservative    8;  Mismatches   17;  Indels   19;  Gaps    4;

Qy         34 PKGKQKAQLRQREVVDLYNG----------MCLQGPAGVPGRDGSPGANVIP------G 76
              |||  | :  : |:|| |||          : | || |:||: | |||  ||      |
Db        431 PKG-SKGEPGKGEMVD-YNGNINEALQEIRTLALMGPPGLPGQIGPPGAPGIPGQKGEIG 488

Qy         77 TPGIPGRDGFKGEKGE 92
              || || || || :|:
Db        489 LPGPPGHDGEKGPRGK 504


RESULT 7
Q90ZA0
ID   Q90ZA0      PRELIMINARY;      PRT;  1472 AA.
AC   Q90ZA0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Collagen type XX alpha 1 precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21303548; PubMed=11274142;
RA   Koch M., Foley J.E., Hahn R., Zhou P., Burgeson R.E., Gerecke D.R.,
RA   Gordon M.K.;
RT   "alpha 1(XX) Collagen, a New Member of the Collagen Subfamily, Fibril-
RT   associated Collagens with Interrupted Triple Helices.";
RL   J. Biol. Chem. 276:23120-23126(2001).
DR   EMBL; AF312825; AAK58847.1; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003129; TSPN.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF01391; Collagen; 4.
DR   Pfam; PF00041; fn3; 6.
DR   Pfam; PF02210; TSPN; 1.
DR   Pfam; PF00092; vwa; 1.
DR   PRINTS; PR00453; VWFADOMAIN.
DR   ProDom; PD000007; Collagen; 1.
```

```
DR   SMART; SM00060; FN3; 6.
DR   SMART; SM00210; TSPN; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Collagen; Signal.
FT   SIGNAL       1     28       POTENTIAL.
SQ   SEQUENCE   1472 AA;  156903 MW;  5361611579C56EFD CRC64;

  Query Match             9.4%;  Score 122.5;  DB 13;  Length 1472;
  Best Local Similarity   33.6%;  Pred. No. 0.0068;
  Matches   37;  Conservative    7;  Mismatches   27;  Indels   39;  Gaps    6;

Qy          3 PQGPAASPQRLRGLLLLLLLQLP-----------APSSASEI----PKGKQKAQLRQREV 47
              | ||  || | ||          |             |    ::    | |:| :   |
Db       1161 PPGPPGSPGR-RG---------PQGEQGEPGPKGEPGPPGKVGPAGPSGQQGSPGSQ--- 1207

Qy         48 VDLYNGMCLQGPAGVP------GRDGSPGANVIPGTPGIPGRDGFKGEKG 91
                |: :||| | |       |  ||||   |||  | ||||| :| ||
Db       1208 -----GITIQGPVGPPGIKGEKGDTGSPGMQGIPGVQGAPGRDGLQGAKG 1252


RESULT 8
Q8CFR0
ID   Q8CFR0      PRELIMINARY;      PRT;   287 AA.
AC   Q8CFR0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to C1q-like.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC040774; AAH40774.1; -.
SQ   SEQUENCE   287 AA;  29292 MW;  8FF89EC1C7420415 CRC64;

  Query Match             9.2%;  Score 120;  DB 11;  Length 287;
  Best Local Similarity   34.7%;  Pred. No. 0.0015;
  Matches   42;  Conservative   10;  Mismatches   57;  Indels   12;  Gaps    4;

Qy         27 PSSASEIPKGKQKAQLRQREVV-DLYNG---MCLQGPAGVPGRDGSPGANVIPGTPGIPG 82
              |: |   | |   | |   ||: ||        :||| | ||| | ||    || || ||
Db         44 PAGAKAPPPGPSTAAL---EVMQDLSANPPPPFIQGPKGDPGRPGKPGPRGPPGEPGPPG 100

Qy         83 RDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFS 142
                |  ||||:  |         |  :  : ::   |:  |        |:    |||   ||
Db        101 PRGPPGEKGDSGRPGL-----PGLQLTTSAAGGVGVVSGGTGGGGDTEGEVTSALSAAFS 155

Qy        143 G 143
              |
Db        156 G 156


RESULT 9
Q07265
ID   Q07265      PRELIMINARY;      PRT;  1752 AA.
AC   Q07265;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   3 alpha procollagen.
GN   COLP3ALPHA.
OS   Strongylocentrotus purpuratus (Purple sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Strongylocentrotus.
OX   NCBI_TaxID=7668;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93186842; PubMed=8444899;
RA   Exposito J.-Y., D'Alessio M., Di Liberto M., Ramirez F.;
RT   "Complete primary structure of a sea-urchin type IV collagen and
RT   analysis of the 5' end of its gene.";
RL   J. Biol. Chem. 268:5249-5254(1993).
DR   EMBL; L02917; AAA30039.1; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001442; ProcollagnC4.
DR   Pfam; PF01413; C4; 2.
DR   Pfam; PF01391; Collagen; 25.
DR   ProDom; PD000007; Collagen; 9.
DR   ProDom; PD003923; ProcollagnC4; 1.
DR   SMART; SM00111; C4; 2.
KW   Collagen.
SQ   SEQUENCE   1752 AA;  170210 MW;  1AE5AAA21569346D CRC64;

  Query Match             9.2%;  Score 120;  DB 5;  Length 1752;
  Best Local Similarity   22.4%;  Pred. No. 0.015;
  Matches   46;  Conservative   20;  Mismatches   61;  Indels   78;  Gaps    9;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV 62
              ||||      |          | |      | |                  | |  |
Db       1453 PQGPPGRDGR------------PGPQG----PPG------------------LTGDKGT 1477

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESF------------------EESWT 103
                ||  |:|| : :|| ||: |  ||:|: |:     |                  | |
Db       1478 PGVQGNPGVSGVPGEPGLKGEQGFRGQNGQPGDPGFPGTKGEAGIPGSSSGFFITRHSQT 1537

Qy        104 PNYKQC------SW----------SSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRL 147
                :  ||       |          :   :| ||||   |    ::  | :  ||  ::
Db       1538 TSIPQCPQGTAKMWHGYSLLFVQGNERGHGQDLGKPGSC----LKRFSTMPFLFC-NINN 1592

Qy        148 KCRNACCQRWYFTFNGAECSGPLPI 172
              |  |    : :  :  |   |:|:
Db       1593 VCHVASRNDYSYWLSTTE---PMPM 1614


RESULT 10
Q18799
ID   Q18799      PRELIMINARY;      PRT;   289 AA.
AC   Q18799;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   C53B4.5 protein.
GN   C53B4.5.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Berks M.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z68215; CAA92453.1; -.
DR   WormPep; C53B4.5; CE03091.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR002486; Col_cuticle_N.
DR   Pfam; PF01391; Collagen; 2.
DR   Pfam; PF01484; Col_cuticle_N; 1.
SQ   SEQUENCE   289 AA;  28994 MW;  2999A3FF9CC0B044 CRC64;

  Query Match             9.1%;  Score 119;  DB 5;  Length 289;
  Best Local Similarity   34.5%;  Pred. No. 0.002;
  Matches   29;  Conservative    5;  Mismatches   20;  Indels   30;  Gaps    2;
```

```
Qy          25 PAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGS----------------P 69
               | | |  |  :  |                    :|||| ||:||:               |
Db         203 PQPGSPGEPGRPGQPGS----------------RGPAGQPGKDGAQGGPGEKGANGEPGQP 247

Qy          70 GANVIPGTPGIPGRDGFKGEKGEC 93
               | :  || || |||||  |||| |
Db         248 GRDGQPGRPGQPGRDGHPGEKGVC 271


RESULT 11
O76045
ID   O76045      PRELIMINARY;      PRT;  1461 AA.
AC   O76045;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Pro alpha 1(I) collagen.
GN   COL1A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85130970; PubMed=2857713;
RA   Chu M.L., de Wet W., Bernard M., Ramirez F.;
RT   "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
RT   Promoter structure, AluI repeats, and polymorphic transcripts.";
RL   J. Biol. Chem. 260:2315-2320(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88329734; PubMed=2843432;
RA   D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.;
RT   "Complete nucleotide sequence of the region encompassing the first
RT   twenty-five exons of the human pro alpha 1(I) collagen gene.";
RL   Gene 67:105-115(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89025644; PubMed=3178743;
RA   Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
RA   Jaenisch R., Prockop D.J.;
RT   "Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
RT   of human type I procollagen.";
RL   Biochem. J. 253:919-922(1988).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91138770; PubMed=1995349;
RA   Maatta A., Bornstein P., Penttinen R.P.;
RT   "Highly conserved sequences in the 3'-untranslated region of the
RT   COL1A1 gene bind cell-specific nuclear proteins.";
RL   FEBS Lett. 279:9-13(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92157916; PubMed=1787829;
RA   Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning C.,
RA   Olsen A.S., Prockop D.J.;
RT   "Completion of the last half of the structure of the human gene for
RT   the Pro alpha 1 (I) chain of type I procollagen (COL1A1).";
RL   Matrix 11:375-379(1991).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98107942; PubMed=9443882;
RA   Korkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,
RA   Prockop D.J.;
RT   "Analysis of the COL1A1 and COL1A2 genes by PCR amplification and
RT   scanning by conformation-sensitive gel electrophoresis identifies only
RT   COL1A1 mutations in 15 patients with osteogenesis imperfecta type I:
RT   identification of common sequences of null-allele mutations.";
RL   Am. J. Hum. Genet. 62:98-110(1998).
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Korkko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
RA   Ala-Kokko L.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF017178; AAB94054.2; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF01410; COLFI; 1.
DR   Pfam; PF01391; Collagen; 18.
DR   Pfam; PF00093; vwc; 1.
DR   ProDom; PD000007; Collagen; 2.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01208; VWFC; 1.
KW   Collagen.
SQ   SEQUENCE   1461 AA;  138630 MW;  9ACF6DE30EA78E21 CRC64;

  Query Match             9.1%;  Score 118.5;  DB 4;  Length 1461;
  Best Local Similarity   36.3%;  Pred. No. 0.017;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy           3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
               ||||  |  || :||         | |      | |                     |||
Db         354 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 382

Qy          61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
               | || || |||    | ||| |  || | :|
Db         383 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 413


RESULT 12
Q8N473
ID   Q8N473      PRELIMINARY;      PRT;  1464 AA.
AC   Q8N473;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC036531; AAH36531.1; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF01410; COLFI; 1.
DR   Pfam; PF01391; Collagen; 18.
DR   ProDom; PD000007; Collagen; 2.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01208; VWFC; 1.
KW   Hypothetical protein; Collagen.
SQ   SEQUENCE   1464 AA;  139011 MW;  B0581F8D1C89DDE8 CRC64;

  Query Match             9.1%;  Score 118.5;  DB 4;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.017;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy           3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
               ||||  |  || :||         | |      | |                     |||
Db         357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy          61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
               | || || |||    | ||| |  || | :|
Db         386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416
```

```
RESULT 13
Q9NAR3
ID   Q9NAR3      PRELIMINARY;      PRT;   291 AA.
AC   Q9NAR3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   C24F3.6 protein.
GN   C24F3.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   McMurray A.A.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; AL022716; CAB97232.1; -.
DR   WormPep; C24F3.6; CE18523.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR002486; Col_cuticle_N.
DR   InterPro; IPR002965; P_rich_extensn.
DR   Pfam; PF01391; Collagen; 2.
DR   Pfam; PF01484; Col_cuticle_N; 1.
DR   PRINTS; PR01217; PRICHEXTENSN.
DR   ProDom; PD000007; Collagen; 2.
KW   Collagen.
SQ   SEQUENCE   291 AA;  29191 MW;  8A8F3685823A3534 CRC64;

  Query Match             9.1%;  Score 118;  DB 5;  Length 291;
  Best Local Similarity   34.5%;  Pred. No. 0.0025;
  Matches   29;  Conservative    6;  Mismatches   19;  Indels   30;  Gaps    2;

Qy         25 PAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGA---------- 71
              | | :  |  :  |  |                :|||| ||:|||||
Db        205 PQPGAPGEPGQPGQPGQ--------------RGPAGEPGKDGSPGGQGEKGASGEPGQP 249

Qy         72 --NVIPGTPGIPGRDGFKGEKGEC 93
                :  || || ||:||  |||| |
Db        250 GRDGQPGHPGQPGKDGRPGEKGVC 273


RESULT 14
Q96JF7
ID   Q96JF7      PRELIMINARY;      PRT;   832 AA.
AC   Q96JF7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein KIAA1870 (Fragment).
GN   KIAA1870.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21245130; PubMed=11347906;
RA   Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XX.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large Proteins in vitro.";
RL   DNA Res. 8:85-95(2001).
DR   EMBL; AB058773; BAB47499.1; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   Pfam; PF01410; COLFI; 1.
DR   Pfam; PF01391; Collagen; 9.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   832 AA;  83207 MW;  527640BD635A337F CRC64;

  Query Match             9.1%;  Score 118;  DB 4;  Length 832;
  Best Local Similarity   47.8%;  Pred. No. 0.0092;
  Matches   33;  Conservative    4;  Mismatches   26;  Indels    6;  Gaps    3;

Qy         25 PAPSSASEIPKGKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIPGTPGIPGR 83
              | | :| ||||| ||    | |    | | || || || | |   | | |:|||
Db        367 PKGSKGAEGPKGKQGKAGAPGRRGVQGLQG--LPGPRGVVGRQGLEG---IAGPDGLPGR 421

Qy         84 DGFKGEKGE 92
              ||  |::||
Db        422 DGQAGQQGE 430


RESULT 15
Q8IZC6
ID   Q8IZC6      PRELIMINARY;      PRT;  1860 AA.
AC   Q8IZC6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Collagen XXVII proalpha 1 chain precursor.
GN   COL27A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cartilage;
RA   Pace J.M., Corrado M., Missero C., Byers P.H.;
RT   "Identification, characterization and expression analysis of a new
RT   fibrillar collagen gene, COL27A1.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY149237; AAN41263.1; -.
KW   Signal.
FT   SIGNAL       1     41       POTENTIAL.
FT   CHAIN      625   1621       COLLAGEN XXVII PROALPHA 1 CHAIN.
SQ   SEQUENCE  1860 AA;  186891 MW;  5F8CDFAF4B6014EC CRC64;

  Query Match             9.1%;  Score 118;  DB 4;  Length 1860;
  Best Local Similarity   47.8%;  Pred. No. 0.025;
  Matches   33;  Conservative    4;  Mismatches   26;  Indels    6;  Gaps    3;

Qy         25 PAPSSASEIPKGKQ-KAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIPGTPGIPGR 83
              | | :| ||||| ||    | |    | | || || || | |   | | |:|||
Db       1395 PKGSKGAEGPKGKQGKAGAPGRRGVQGLQG--LPGPRGVVGRQGLEG---IAGPDGLPGR 1449

Qy         84 DGFKGEKGE 92
              ||  |::||
Db       1450 DGQAGQQGE 1458


Search completed: August 13, 2003, 13:27:21
Job time : 98 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:15:46 ; Search time 23 Seconds
(without alignments)
496.847 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	122.5	9.4	246	1	C1QC_MOUSE	Q02105 mus musculu
2	118.5	9.1	1464	1	CA11_HUMAN	P02452 homo sapien
3	117	9.0	754	1	CA54_CANFA	Q28247 canis famil
4	116	8.9	1670	1	CA34_HUMAN	Q01955 homo sapien
5	116	8.9	1685	1	CA54_HUMAN	P29400 homo sapien
6	115.5	8.9	289	1	CQT7_HUMAN	Q9bxj2 homo sapien
7	115.5	8.9	1516	1	CA1H_HUMAN	P39060 homo sapien
8	115.5	8.9	1669	1	CA14_HUMAN	P02462 homo sapien
9	115	8.8	1466	1	CA13_HUMAN	P02461 homo sapien
10	115	8.8	1763	1	CA24_ASCSU	P27393 ascaris suu
11	113.5	8.7	1691	1	CA64_HUMAN	Q14031 homo sapien
12	113	8.7	2944	1	CA17_HUMAN	Q02388 homo sapien
13	112	8.6	245	1	C1QC_HUMAN	P02747 homo sapien
14	111	8.5	747	1	CA12_BOVIN	P02459 bos taurus
15	110.5	8.5	671	1	CA11_RAT	P02454 rattus norv
16	110.5	8.5	1453	1	CA11_MOUSE	P11087 mus musculu
17	110.5	8.5	1460	1	CA11_CANFA	Q9xsj7 canis famil
18	110	8.5	258	1	C1RF_HUMAN	O75973 homo sapien
19	110	8.5	299	1	CC34_CAEEL	P34687 caenorhabdi
20	110	8.5	684	1	CA39_HUMAN	Q14050 homo sapien
21	110	8.5	1049	1	CA13_BOVIN	P04258 bos taurus
22	110	8.5	1453	1	CA11_CHICK	P02457 gallus gall
23	110	8.5	1806	1	CA1B_HUMAN	P12107 homo sapien
24	109	8.4	1669	1	CA14_MOUSE	P02463 mus musculu
25	109	8.4	1758	1	CA14_CAEEL	P17139 caenorhabdi
26	108.5	8.3	1418	1	CA12_HUMAN	P02458 homo sapien
27	108.5	8.3	1459	1	CA12_MOUSE	P28481 mus musculu
28	107	8.2	744	1	CA18_HUMAN	P27658 homo sapien
29	107	8.2	765	1	KF10_MOUSE	Q923p0 mus musculu
30	106.5	8.2	453	1	MSRE_BOVIN	P21758 bos taurus
31	106.5	8.2	743	1	CA18_MOUSE	Q00780 mus musculu
32	106.5	8.2	779	1	CA11_BOVIN	P02453 bos taurus
33	106.5	8.2	1262	1	CA13_CHICK	P12105 gallus gall
34	106.5	8.2	1464	1	CA13_MOUSE	P08121 mus musculu
35	106.5	8.2	1758	1	CA24_CAEEL	P17140 caenorhabdi
36	106	8.1	296	1	CC01_CAEEL	P08124 caenorhabdi
37	106	8.1	301	1	CC02_CAEEL	P17656 caenorhabdi
38	106	8.1	302	1	CCDC_CAEEL	P17657 caenorhabdi
39	106	8.1	482	1	CA1B_RAT	P20909 rattus norv
40	106	8.1	744	1	CA18_RABIT	P14282 oryctolagus
41	106	8.1	1143	1	CA1I_HUMAN	Q14993 homo sapien
42	106	8.1	1804	1	CA1B_MOUSE	Q61245 mus musculu
43	105.5	8.1	283	1	YQ33_CAEEL	Q09233 caenorhabdi
44	105.5	8.1	674	1	CA1A_BOVIN	P23206 bos taurus
45	105.5	8.1	674	1	CA1A_CHICK	P08125 gallus gall

ALIGNMENTS

```
RESULT 1
C1QC_MOUSE
ID   C1QC_MOUSE     STANDARD;      PRT;   246 AA.
AC   Q02105;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Complement C1q subcomponent, C chain precursor.
GN   C1QG OR C1QC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=Macrophage;
RX   MEDLINE=93011118; PubMed=1396691;
RA   Petry F., Reid K.B.M., Loos M.;
RT   "Isolation, sequence analysis and characterization of cDNA clones
RT   coding for the C chain of mouse C1q. Sequence similarity of
RT   complement subcomponent C1q, collagen type VIII and type X and
RT   precerebellin.";
RL   Eur. J. Biochem. 209:129-134(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=96186528; PubMed=8606057;
RA   Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;
RT   "The mouse C1q genes are clustered on chromosome 4 and show
RT   conservation of gene organization.";
RL   Immunogenetics 43:370-376(1996).
CC   -!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD
CC       C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
CC       COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT
CC       C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1
CC       TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
CC       FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
CC   -!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
CC       AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED
CC       OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
CC       A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF
CC       THE C CHAIN.
CC   -!- SIMILARITY: Contains 1 collagenous domain.
CC   -!- SIMILARITY: Contains 1 C1Q domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X66295; CAA46993.1; -.
DR   EMBL; X92960; CAA63535.1; -.
DR   PIR; S29328; S29328.
```

```
DR   MGD; MGI:88225; C1qg.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 1.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   ProDom; PD000007; C1g_helix; 1.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
KW   Repeat; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    246       COMPLEMENT C1Q SUBCOMPONENT, C CHAIN.
FT   DOMAIN       32    113       COLLAGEN-LIKE.
FT   DOMAIN      114    246       C1Q.
FT   DISULFID     33     33       INTERCHAIN (WITH OTHER C CHAIN)
FT                                (BY SIMILARITY).
FT   MOD_RES      37     37       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      40     40       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      43     43       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      61     61       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      64     64       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      73     73       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      76     76       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      79     79       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      82     82       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES      97     97       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES     100    100       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES     106    106       HYDROXYLATION (BY SIMILARITY).
FT   MOD_RES     109    109       HYDROXYLATION (BY SIMILARITY).
SQ   SEQUENCE   246 AA;  25966 MW;  2F79EA1274BCB8E0 CRC64;

  Query Match             9.4%;  Score 122.5;  DB 1;  Length 246;
  Best Local Similarity   37.4%;  Pred. No. 0.00072;
  Matches   34;  Conservative    5;  Mismatches   33;  Indels   19;  Gaps    2;

Qy          5 GPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
              ||:  ||    |||| || ||  | ||                  |    : |  | ||
Db          4 GPSCQPQCGLCLLLLFLLALPLRSQAS----------------AGCYGIPGMPGMPGAPG 47

Qy         65 RDGS---PGANVIPGTPGIPGRDGFKGEKGE 92
              :||     |    || | :||  | ||:|||
Db         48 KDGHDGLQGPKGEPGIPAVPGTQGPKGQKGE 78


RESULT 2
CA11_HUMAN
ID   CA11_HUMAN     STANDARD;      PRT;  1464 AA.
AC   P02452; Q14037; Q15176;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 1(I) chain precursor.
GN   COL1A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-472 FROM N.A.
RX   MEDLINE=89025644; PubMed=3178743;
RA   Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
RA   Jaenisch R., Prockup D.J.;
RT   "Structure of a full-length cDNA clone for the prepro alpha 1(I)
RT   chain of human type I procollagen.";
RL   Biochem. J. 253:919-922(1988).
RN   [2]
RP   SEQUENCE OF 1-181 FROM N.A.
RX   MEDLINE=84270697; PubMed=6462220;
RA   Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
RA   Myers J., Williams C., Ramirez F.;
RT   "Human pro alpha 1(I) collagen gene structure reveals evolutionary
RT   conservation of a pattern of introns and exons.";
RL   Nature 310:337-340(1984).
RN   [3]
RP   SEQUENCE OF 162-301.
RC   TISSUE=Skin;
RX   MEDLINE=71038625; PubMed=5529814;
RA   Click E.M., Bornstein P.;
RT   "Isolation and characterization of the cyanogen bromide peptides from
RT   the alpha 1 and alpha 2 chains of human skin collagen.";
RL   Biochemistry 9:4699-4706(1970).
RN   [4]
RP   SEQUENCE OF 263-268.
RC   TISSUE=Skin;
RX   MEDLINE=71001508; PubMed=4319110;
RA   Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
RT   "A comparative study of glycopeptides derived from selected
RT   vertebrate collagens. A possible role of the carbohydrate in fibril
RT   formation.";
RL   J. Biol. Chem. 245:5042-5048(1970).
RN   [5]
RP   SEQUENCE OF 425-1464 FROM N.A.
RX   MEDLINE=84080385; PubMed=6689127;
RA   Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
RA   Prockop D.J.;
RT   "Nucleotide sequences of complementary deoxyribonucleic acids for the
RT   pro alpha 1 chain of human type I procollagen. Statistical evaluation
RT   of structures that are conserved during evolution.";
RL   Biochemistry 22:5213-5223(1983).
RN   [6]
RP   SEQUENCE OF 1229-1454 FROM N.A.
RC   TISSUE=Bone;
RX   MEDLINE=88124208; PubMed=3340531;
RA   Maekelae J.K., Raassina M., Virta A., Vuorio E.;
RT   "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
RT   domain.";
RL   Nucleic Acids Res. 16:349-349(1988).
RN   [7]
RP   SEQUENCE OF 1-34 FROM N.A.
RX   MEDLINE=88097389; PubMed=3480516;
RA   Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
RT   "Regulatory elements in the first intron contribute to
RT   transcriptional control of the human alpha 1(I) collagen gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
RN   [8]
RP   SEQUENCE OF 1-34 FROM N.A.
RX   MEDLINE=85130970; PubMed=2857713;
RA   Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
RT   "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
RT   Promoter structure, AluI repeats, and polymorphic transcripts.";
RL   J. Biol. Chem. 260:2315-2320(1985).
RN   [9]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE=88033098; PubMed=2822714;
RA   Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
RA   de Wet W.J.;
RT   "DNA sequences in the first intron of the human pro-alpha 1(I)
RT   collagen gene enhance transcription.";
RL   J. Biol. Chem. 262:15151-15157(1987).
RN   [10]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=91184577; PubMed=2010058;
RA   Kuivaniemi H., Tromp G., Prockop D.J.;
RT   "Mutations in collagen genes: causes of rare and some common diseases
RT   in humans.";
RL   FASEB J. 5:2052-2060(1991).
RN   [11]
RP   REVIEW ON VARIANTS.
RX   MEDLINE=97255959; PubMed=9101290;
RA   Kuivaniemi H., Tromp G., Prockop D.J.;
RT   "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT   associated collagen (type IX), and network-forming collagen (type X)
RT   cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL   Hum. Mutat. 9:300-315(1997).
RN   [12]
```

```
RP   REVIEW ON OI VARIANTS.
RX   MEDLINE=91374476; PubMed=1895312;
RA   Byers P.H., Wallis G.A., Willing M.C.;
RT   "Osteogenesis imperfecta: translation of mutation to phenotype.";
RL   J. Med. Genet. 28:433-442(1991).
RN   [13]
RP   REVIEW ON OI VARIANTS.
RX   MEDLINE=97169389; PubMed=9016532;
RA   Dalgleish R.;
RT   "The human type I collagen mutation database.";
RL   Nucleic Acids Res. 25:181-187(1997).
RN   [14]
RP   VARIANT OI-II CYS-1166.
RX   MEDLINE=86287390; PubMed=3016737;
RA   Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
RT   "Lethal osteogenesis imperfecta resulting from a single nucleotide
RT   change in one human pro alpha 1(I) collagen allele.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
RN   [15]
RP   VARIANT OI-II ARG-569.
RX   MEDLINE=87222295; PubMed=3108247;
RA   Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
RT   "Lethal perinatal osteogenesis imperfecta due to the substitution of
RT   arginine for glycine at residue 391 of the alpha 1(I) chain of type I
RT   collagen.";
RL   J. Biol. Chem. 262:7021-7027(1987).
RN   [16]
RP   VARIANT OI-II CYS-926.
RX   MEDLINE=88033031; PubMed=3667599;
RA   Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
RT   "A point mutation in a type I procollagen gene converts glycine 748
RT   of the alpha 1 chain to cysteine and destabilizes the triple helix in
RT   a lethal variant of osteogenesis imperfecta.";
RL   J. Biol. Chem. 262:14737-14744(1987).
RN   [17]
RP   VARIANT OI-II ARG-842.
RX   MEDLINE=88298828; PubMed=3403550;
RA   Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;
RT   "Substitution of arginine for glycine 664 in the collagen alpha 1(I)
RT   chain in lethal perinatal osteogenesis imperfecta. Demonstration of
RT   the peptide defect by in vitro expression of the mutant cDNA.";
RL   J. Biol. Chem. 263:11627-11630(1988).
RN   [18]
RP   VARIANT OI CYS-1195.
RX   MEDLINE=89218628; PubMed=3244312;
RA   Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
RT   "A cysteine for glycine substitution at position 1017 in an alpha
RT   1(I) chain of type I collagen in a patient with mild dominantly
RT   inherited osteogenesis imperfecta.";
RL   Mol. Biol. Med. 5:197-207(1988).
RN   [19]
RP   VARIANT OI-II VAL-434.
RX   MEDLINE=89255493; PubMed=2470760;
RA   Patterson E., Smiley E., Bonadio J.;
RT   "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
RT   mutation.";
RL   J. Biol. Chem. 264:10083-10087(1989).
RN   [20]
RP   VARIANT OI-IV SER-1010.
RX   MEDLINE=89308591; PubMed=2745420;
RA   Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koeplin D.A.;
RT   "Osteogenesis imperfecta type IV. Detection of a point mutation in
RT   one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";
RL   J. Biol. Chem. 264:11893-11900(1989).
RN   [21]
RP   VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
RX   MEDLINE=89380165; PubMed=2777764;
RA   Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
RT   "Characterization of point mutations in the collagen COL1A1 and
RT   COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";
RL   J. Biol. Chem. 264:15809-15812(1989).
RN   [22]
RP   VARIANT OI SER-1022.
RX   MEDLINE=90062068; PubMed=2511192;
RA   Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
RT   "Substitution of serine for alpha 1(I)-glycine 844 in a severe
RT   variant of osteogenesis imperfecta minimally destabilizes the triple
RT   helix of type I procollagen. The effects of glycine substitutions on
RT   thermal stability are either position of amino acid specific.";
RL   J. Biol. Chem. 264:19694-19699(1989).
RN   [23]
RP   VARIANT OI-II CYS-1082.
RX   MEDLINE=89109573; PubMed=2913053;
RA   Constantinou C.D., Nielsen K.B., Prockop D.J.;
RT   "A lethal variant of osteogenesis imperfecta has a single base
RT   mutation that substitutes cysteine for glycine 904 of the alpha 1(I)
RT   chain of type I procollagen. The asymptomatic mother has an
RT   unidentified mutation producing an overmodified and unstable type I
RT   procollagen.";
RL   J. Clin. Invest. 83:574-584(1989).
RN   [24]
RP   VARIANTS OI CYS-272; CYS-704 AND CYS-896.
RX   MEDLINE=90009313; PubMed=2794057;
RA   Starman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,
RA   Weiss L., Graham J.M., Byers P.H.;
RT   "Osteogenesis imperfecta. The position of substitution for glycine by
RT   cysteine in the triple helical domain of the pro alpha 1(I) chains of
RT   type I collagen determines the clinical phenotype.";
RL   J. Clin. Invest. 84:1206-1214(1989).
RN   [25]
RP   VARIANT OI-II CYS-422.

  Query Match             9.1%;  Score 118.5;  DB 1;  Length 1464;
  Best Local Similarity   36.3%;  Pred. No. 0.013;
  Matches   33;  Conservative    2;  Mismatches   23;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||        | |      | |                     |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 3
CA54_CANFA
ID   CA54_CANFA     STANDARD;      PRT;   754 AA.
AC   Q28247;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 5(IV) chain (Fragment).
GN   COL4A5.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Samoyed; TISSUE=Kidney;
RX   MEDLINE=94224868; PubMed=8171024;
RA   Zheng K., Thorner P.S., Marrano P., Baumal R., McInnes R.R.;
RT   "Canine X chromosome-linked hereditary nephritis: a genetic model for
RT   human X-linked hereditary nephritis resulting from a single base
RT   mutation in the gene encoding the alpha 5 chain of collagen type
RT   IV.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3989-3993(1994).
CC   -!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF
CC       GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
CC       MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
CC       NIDOGEN.
CC   -!- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
CC       ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
CC       WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
CC   -!- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
```

```
CC   -!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
CC       DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
CC       G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CC       CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
CC       TRIPLE-HELICAL 7S DOMAIN.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- PTM: Type IV collagens contain numerous cysteine residues which
CC       are involved in inter- and intramolecular disulfide bonding. 12 of
CC       these, located in the NC1 domain, are conserved in all known type
CC       IV collagens.
CC   -!- DISEASE: A DEFECT IN COL4A5 HAS BEEN FOUND TO BE THE CAUSE OF
CC       CANINE X-LINKED HEREDITARY NEPHRITIS (HN), A DISEASE SIMILAR TO
CC       THAT IN HUMANS (ALSO REFERRED TO AS ALPORT SYNDROME) CHARACTERIZED
CC       BY PROGRESSIVE RENAL FAILURE AND NEUROSENSORY DEAFNESS.
CC   -!- SIMILARITY: TO OTHER TYPE IV COLLAGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U07888; AAB60258.1; -.
DR   PIR; A55267; A55267.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001442; ProcollagnC4.
DR   Pfam; PF01413; C4; 2.
DR   Pfam; PF01391; Collagen; 8.
DR   ProDom; PD000007; Clg_helix; 1.
DR   ProDom; PD003923; ProcollagnC4; 1.
DR   SMART; SM00111; C4; 2.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Glycoprotein; Basement membrane; Collagen; Cell adhesion.
FT   NON_TER       1      1
FT   DOMAIN       <1    530       TRIPLE-HELICAL REGION.
FT   DOMAIN      531   >754       NONHELICAL REGION (NC1).
FT   DISULFID    552    643       OR 640 (BY SIMILARITY).
FT   DISULFID    585    640       OR 643 (BY SIMILARITY).
FT   DISULFID    597    603       BY SIMILARITY.
FT   DISULFID    662      ?       OR 754 (BY SIMILARITY).
FT   DISULFID    696    754       BY SIMILARITY.
FT   DISULFID    708    714       BY SIMILARITY.
FT   NON_TER     754    754
SQ   SEQUENCE   754 AA;  73537 MW;  D5E321C287FA925B CRC64;

  Query Match             9.0%;  Score 117;  DB 1;  Length 754;
  Best Local Similarity   34.4%;  Pred. No. 0.0084;
  Matches   33;  Conservative    7;  Mismatches   34;  Indels   22;  Gaps    4;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIP-----KGKQ--KAQLRQREVVDLYNGMC 55
              ||||   |             || |     :|     ||::    |  |  :  |
Db        332 PQGPPGRP-----------GLPGPEGPRGLPGNGGIKGERGNPGQPGQPGLPGLKGD-- 377

Qy         56 LQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
               ||| |: |  | || | : | ||:||  || | ||
Db        378 -QGPPGIQGNPGRPGLNGMKGDPGLPGVPGFPGMKG 412


RESULT 4
CA34_HUMAN
ID   CA34_HUMAN     STANDARD;      PRT;  1670 AA.
AC   Q01955; Q9BQT2;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 3(IV) chain precursor (Goodpasture antigen).
GN   COL4A3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=94364994; PubMed=8083201;
RA   Mariyama M., Leinonen A., Mochizuki T., Tryggvason K., Reeders S.T.;
RT   "Complete primary structure of the human alpha 3(IV) collagen chain.
RT   Coexpression of the alpha 3(IV) and alpha 4(IV) collagen chains in
RT   human tissues.";
RL   J. Biol. Chem. 269:23013-23017(1994).
RN   [2]
RP   REVISIONS.
RA   Leinonen A.;
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A., VARIANTS AS GLU-297; ARG-407; ARG-640; ARG-1167;
RP   GLU-1207; GLN-1215; SER-1277; THR-1330; GLU-1334; GLU-1347 AND
RP   CYS-1661, AND VARIANTS ARG-43; GLU-162; TYR-326; HIS-408; ARG-451;
RP   PRO-574; GLU-1269 AND PRO-1474.
RX   MEDLINE=21064696; PubMed=11134255;
RA   Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Mollet G.,
RA   Gutierrez B., Stavrou C., Gubler M.C., Antignac C.;
RT   "Structure of the human type IV collagen gene COL4A3 and mutations in
RT   autosomal Alport syndrome.";
RL   J. Am. Soc. Nephrol. 12:97-106(2001).
RN   [4]
RP   SEQUENCE OF 1386-1670 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=93015826; PubMed=1400291;
RA   Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.;
RT   "Exon/intron structure of the human alpha 3(IV) gene encompassing the
RT   Goodpasture antigen (alpha 3(IV)NC1). Identification of a potentially
RT   antigenic region at the triple helix/NC1 domain junction.";
RL   J. Biol. Chem. 267:19780-19784(1992).
RN   [5]
RP   SEQUENCE OF 1453-1670 FROM N.A.
RX   MEDLINE=91353570; PubMed=1882840;
RA   Morrison K.E., Mariyama M., Yang-Feng T.L., Reeders S.T.;
RT   "Sequence and localization of a partial cDNA encoding the human alpha
RT   3 chain of type IV collagen.";
RL   Am. J. Hum. Genet. 49:545-554(1991).
RN   [6]
RP   SEQUENCE OF 1331-1670 FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92147878; PubMed=1737849;
RA   Turner N., Mason P.J., Brown R., Fox M., Povey S., Rees A.,
RA   Pusey C.D.;
RT   "Molecular cloning of the human Goodpasture antigen demonstrates it
RT   to be the alpha 3 chain of type IV collagen.";
RL   J. Clin. Invest. 89:592-601(1992).
RN   [7]
RP   SEQUENCE OF 1644-1670 FROM N.A.
RC   TISSUE=Kidney;
RA   Ding J.;
RL   Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 1439-1670, AND ALTERNATIVE SPLICING.
RC   TISSUE=Kidney;
RX   MEDLINE=94124597; PubMed=8294492;
RA   Feng L., Xia Y., Wilson C.B.;
RT   "Alternative splicing of the NC1 domain of the human alpha 3(IV)
RT   collagen gene. Differential expression of mRNA transcripts that
RT   predict three protein variants with distinct carboxyl regions.";
RL   J. Biol. Chem. 269:2342-2348(1994).
RN   [9]
RP   SEQUENCE OF 1-29 FROM N.A.
RX   MEDLINE=98196854; PubMed=9537506;
RA   Momota R., Sugimoto M., Oohashi T., Kigasawa K., Yoshioka H.,
RA   Ninomiya Y.;
RT   "Two genes, COL4A3 and COL4A4 coding for the human alpha3(IV) and
RT   alpha4(IV) collagen chains are arranged head-to-head on chromosome
RT   2q36.";
RL   FEBS Lett. 424:11-16(1998).
RN   [10]
```

```
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=93280184; PubMed=8505332;
RA   Bernal D., Quinones S., Saus J.;
RT   "The human mRNA encoding the Goodpasture antigen is alternatively
RT   spliced.";
RL   J. Biol. Chem. 268:12090-12094(1993).
RN   [11]
RP   VARIANT PRO-1474.
RX   MEDLINE=95078827; PubMed=7987301;
RA   Lemmink H.H., Mochizuki T., van den Heuvel L.P.W.J., Schroeder C.H.,
RA   Barrientos A., Monnens L.A.H., van Oost B.A., Brunner H.G.,
RA   Reeders S.T., Smeets H.J.M.;
RT   "Mutations in the type IV collagen alpha 3 (COL4A3) gene in autosomal
RT   recessive Alport syndrome.";
RL   Hum. Mol. Genet. 3:1269-1273(1994).
CC   -!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF
CC       GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
CC       MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
CC       NIDOGEN.
CC   -!- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
CC       ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH
CC       2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
CC   -!- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist. Isoforms differ in
CC         the C-terminal part of the NC1 domain;
CC       Name=1;
CC         IsoId=Q01955-1; Sequence=Displayed;
CC       Name=2; Synonyms=V;
CC         IsoId=Q01955-2; Sequence=VSP_001170;
CC       Name=3; Synonyms=L5;
CC         IsoId=Q01955-3; Sequence=VSP_001171;
CC   -!- TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS ARE
CC       COLOCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE,
CC       COCHLEA, LUNG AND BRAIN.
CC   -!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
CC       DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
CC       G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CC       CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
CC       TRIPLE-HELICAL 7S DOMAIN.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- PTM: Isoform 2 contains an additional N-linked glycosylation site.
CC   -!- PTM: Type IV collagens contain numerous cysteine residues which
CC       are involved in inter- and intramolecular disulfide bonding. 12 of
CC       these, located in the NC1 domain, are conserved in all known type
CC       IV collagens.
CC   -!- PTM: Phosphorylated by the Goodpasture antigen-binding protein.
CC   -!- DISEASE: Antibodies against the NC1 domain of alpha3(IV) mediate
CC       the autoimmune disease Goodpasture syndrome [MIM:233450], which is
CC       characterized by hematuria and pulmonary hemorrhage.
CC   -!- DISEASE: Defects in COL4A3 are a cause of autosomal recessive
CC       Alport syndrome (AS) [MIM:203780], an hereditary disorder
CC       characterized by progressive glomerulonephritis, renal failure,
CC       hematuria, ocular abnormalities and deafness. The recessive form
CC       occurs equally between males and females.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80031; CAA56335.1; -.
DR   EMBL; AJ288487; CAC36101.1; -.
DR   EMBL; AJ288488; CAC36101.1; JOINED.
DR   EMBL; AJ288489; CAC36101.1; JOINED.
DR   EMBL; AJ288490; CAC36101.1; JOINED.
DR   EMBL; AJ288491; CAC36101.1; JOINED.
DR   EMBL; AJ288492; CAC36101.1; JOINED.
DR   EMBL; AJ288493; CAC36101.1; JOINED.
DR   EMBL; AJ288494; CAC36101.1; JOINED.
DR   EMBL; AJ288495; CAC36101.1; JOINED.
DR   EMBL; AJ288496; CAC36101.1; JOINED.
DR   EMBL; AJ288497; CAC36101.1; JOINED.
DR   EMBL; AJ288498; CAC36101.1; JOINED.
DR   EMBL; AJ288499; CAC36101.1; JOINED.
DR   EMBL; AJ288500; CAC36101.1; JOINED.
DR   EMBL; AJ288501; CAC36101.1; JOINED.
DR   EMBL; AJ288502; CAC36101.1; JOINED.
DR   EMBL; AJ288503; CAC36101.1; JOINED.
DR   EMBL; AJ288504; CAC36101.1; JOINED.
DR   EMBL; AJ288505; CAC36101.1; JOINED.
DR   EMBL; AJ288506; CAC36101.1; JOINED.
DR   EMBL; AJ288507; CAC36101.1; JOINED.
DR   EMBL; AJ288508; CAC36101.1; JOINED.
DR   EMBL; AJ288509; CAC36101.1; JOINED.
DR   EMBL; AJ288510; CAC36101.1; JOINED.
DR   EMBL; AJ288511; CAC36101.1; JOINED.
DR   EMBL; AJ288512; CAC36101.1; JOINED.
DR   EMBL; AJ288513; CAC36101.1; JOINED.
DR   EMBL; AJ288514; CAC36101.1; JOINED.
DR   EMBL; AJ288515; CAC36101.1; JOINED.
DR   EMBL; AJ288516; CAC36101.1; JOINED.
DR   EMBL; AJ288517; CAC36101.1; JOINED.
DR   EMBL; AJ288518; CAC36101.1; JOINED.
DR   EMBL; AJ288519; CAC36101.1; JOINED.
DR   EMBL; AJ288520; CAC36101.1; JOINED.
DR   EMBL; AJ288521; CAC36101.1; JOINED.
DR   EMBL; AJ288522; CAC36101.1; JOINED.
DR   EMBL; AJ288523; CAC36101.1; JOINED.
DR   EMBL; AJ288524; CAC36101.1; JOINED.
DR   EMBL; AJ288525; CAC36101.1; JOINED.
DR   EMBL; AJ288526; CAC36101.1; JOINED.
DR   EMBL; AJ288527; CAC36101.1; JOINED.
DR   EMBL; AJ288528; CAC36101.1; JOINED.
DR   EMBL; AJ288529; CAC36101.1; JOINED.
DR   EMBL; AJ288530; CAC36101.1; JOINED.
DR   EMBL; AJ288531; CAC36101.1; JOINED.
DR   EMBL; AJ288532; CAC36101.1; JOINED.
DR   EMBL; AJ288533; CAC36101.1; JOINED.
DR   EMBL; AJ288534; CAC36101.1; JOINED.
DR   EMBL; AJ288535; CAC36101.1; JOINED.
DR   EMBL; AJ288536; CAC36101.1; JOINED.

  Query Match             8.9%;  Score 116;  DB 1;  Length 1670;
  Best Local Similarity   35.1%;  Pred. No. 0.026;
  Matches   33;  Conservative    6;  Mismatches   37;  Indels   18;  Gaps    3;

Qy          5 GPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
              ||   |    |||      :| |     :|       :  |           || ||: |
Db        467 GPKGEP----GLLCTQCPYIPGPPGLPGLPGLHGVKGIPGR----------QGAAGLKG 511

Qy         65 RDGSPGANVIPGTPGIPGRD---GFKGEKGECLR 95
                ||||   :|| || ||    | |||||| |:
Db        512 SPGSPGNTGLPGFPGFPGAQGDPGLKGEKGETLQ 545


RESULT 5
CA54_HUMAN
ID   CA54_HUMAN     STANDARD;      PRT;  1685 AA.
AC   P29400; Q16006; Q16126;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 5(IV) chain precursor.
GN   COL4A5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

RX MEDLINE=94165049; PubMed=8120014;
RA Zhou J., Leinonen A., Tryggvason K.;
RT "Structure of the human type IV collagen COL4A5 gene.";
RL J. Biol. Chem. 269:6608-6614(1994).
RN [2]
RP SEQUENCE OF 1-910 FROM N.A., AND VARIANT AS CYS-521.
RC TISSUE=Kidney;
RX MEDLINE=92316923; PubMed=1352287;
RA Zhou J., Hertz J.M., Leinonen A., Tryggvason K.;
RT "Complete amino acid sequence of the human alpha 5 (IV) collagen
RT chain and identification of a single-base mutation in exon 23
RT converting glycine 521 in the collagenous domain to cysteine in an
RT Alport syndrome patient.";
RL J. Biol. Chem. 267:12475-12481(1992).
RN [3]
RP SEQUENCE OF 85-1685 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90337990; PubMed=2380186;
RA Pihlajaniemi T., Pohjolainen E.R., Myers J.C.;
RT "Complete primary structure of the triple-helical region and the
RT carboxyl-terminal domain of a new type IV collagen chain, alpha
RT 5(IV).";
RL J. Biol. Chem. 265:13758-13766(1990).
RN [4]
RP SEQUENCE OF 924-1685 FROM N.A.
RX MEDLINE=91169491; PubMed=2004755;
RA Zhou J., Hostikka S.L., Chow L.T., Tryggvason K.;
RT "Characterization of the 3' half of the human type IV collagen alpha
RT 5 gene that is affected in the Alport syndrome.";
RL Genomics 9:1-9(1991).
RN [5]
RP SEQUENCE OF 914-1685 FROM N.A.
RX MEDLINE=90160375; PubMed=1689491;
RA Hostikka S.L., Eddy R.L., Byers M.G., Hoeyhtyae M., Shows T.B.,
RA Tryggvason K.;
RT "Identification of a distinct type IV collagen alpha chain with
RT restricted kidney distribution and assignment of its gene to the
RT locus of X chromosome-linked Alport syndrome.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1606-1610(1990).
RN [6]
RP SEQUENCE OF 1442-1471 FROM N.A.
RX MEDLINE=90252791; PubMed=2339699;
RA Myers J.C., Jones T.A., Pohjolainen E.R., Kadri A.S., Goddard A.D.,
RA Sheer D., Solomon E., Pihlajaniemi T.;
RT "Molecular cloning of alpha 5(IV) collagen and assignment of the gene
RT to the region of the X chromosome containing the Alport syndrome
RT locus.";
RL Am. J. Hum. Genet. 46:1024-1033(1990).
RN [7]
RP SEQUENCE OF 1-20 FROM N.A.
RA Guo C., van Damme B., Vanrenterghem Y., Devriendt K., Cassiman J.-J.,
RA Marynen P.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE OF 1258-1270 FROM N.A. (ISOFORM 2).
RX MEDLINE=94133540; PubMed=8301933;
RA Guo C., van Damme B., van Damme-Lombaerts R., van den Berghe H.,
RA Cassiman J.-J., Marynen P.;
RT "Differential splicing of COL4A5 mRNA in kidney and white blood
RT cells: a complex mutation in the COL4A5 gene of an Alport patient
RT deletes the NC1 domain.";
RL Kidney Int. 44:1316-1321(1993).
RN [9]
RP REVIEW ON VARIANTS.
RX MEDLINE=97338662; PubMed=9195222;
RA Lemmink H.H., Schroeder C.H., Monnens L.A.H., Smeets H.J.M.;
RT "The clinical spectrum of type IV collagen mutations.";
RL Hum. Mutat. 9:477-499(1997).
RN [10]
RP VARIANT AS SER-1564.
RX MEDLINE=91169492; PubMed=1672282;
RA Zhou J., Barker D.F., Hostikka S.L., Gregory M.C., Atkin C.L.,
RA Tryggvason K.;
RT "Single base mutation in alpha 5(IV) collagen chain gene converting a
RT conserved cysteine to serine in Alport syndrome.";
RL Genomics 9:10-18(1991).
RN [11]
RP VARIANT AS ARG-325.
RX MEDLINE=92303559; PubMed=1376965;
RA Knebelmann B., Deschenes G., Gros F., Hors M.-C., Gruenfeld J.-P.,
RA Tryggvason K., Gubler M.-C., Antignac C.;
RT "Substitution of arginine for glycine 325 in the collagen alpha 5
RT (IV) chain associated with X-linked Alport syndrome: characterization
RT of the mutation by direct sequencing of PCR-amplified lymphoblast
RT cDNA fragments.";
RL Am. J. Hum. Genet. 51:135-142(1992).
RN [12]
RP VARIANT AS GLU-325.
RX MEDLINE=93244772; PubMed=1363780;
RA Renieri A., Seri M., Myers J.C., Pihlajaniemi T., Massella L.,
RA Rizzoni G.F., de Marchi M.;
RT "De novo mutation in the COL4A5 gene converting glycine 325 to
RT glutamic acid in Alport syndrome.";
RL Hum. Mol. Genet. 1:127-129(1992).
RN [13]
RP VARIANTS AS THR-1517; SER-1538 AND GLN-1563.
RX MEDLINE=94010948; PubMed=8406498;
RA Lemmink H.L., Schroeder C.H., Brunner H.G., Nelen M.R., Zhou J.,
RA Tryggvason K., Haggsma-Schouten W.A.G., Roodvoets A.P., Rascher W.,
RA van Oost B.A., Smeets H.J.M.;
RT "Identification of four novel mutations in the COL4A5 gene of
RT patients with Alport syndrome.";
RL Genomics 17:485-489(1993).
RN [14]
RP VARIANTS AS GLU-400; VAL-406; VAL-638; ALA-638; ARG-653; ARG-796;
RP ARG-869; ARG-872 AND CYS-1241.
RX MEDLINE=95322976; PubMed=7599631;
RA Boye E., Flinter F., Zhou J., Tryggvason K., Bobrow M., Harris A.;
RT "Detection of 12 novel mutations in the collagenous domain of the
RT COL4A5 gene in Alport syndrome patients.";
RL Hum. Mutat. 5:197-204(1995).
RN [15]
RP VARIANT AS ARG-1649.
RX MEDLINE=96213750; PubMed=8651292;
RA Barker D.F., Pruchno C.J., Jiang X., Atkin C.L., Stone E.M.,
RA Denison J.C., Fain P.R., Gregory M.C.;
RT "A mutation causing Alport syndrome with tardive hearing loss is
RT common in the western United States.";
RL Am. J. Hum. Genet. 58:1157-1165(1996).
RN [16]
RP VARIANTS AS.
RX MEDLINE=96213754; PubMed=8651296;
RA Renieri A., Bruttini M., Galli L., Zanelli P., Neri T.M., Rossetti S.,
RA Turco A.E., Heiskari N., Zhou J., Gusmano R., Massella L., Banfi G.,
RA Scolari F., Sessa A., Rizzoni G.F., Tryggvason K., Pignatti P.F.,
RA Savi M., Ballabio A., de Marchi M.;
RT "X-linked Alport syndrome: an SSCP-based mutation survey over all 51
RT exons of the COL4A5 gene.";
RL Am. J. Hum. Genet. 58:1192-1204(1996).
RN [17]
RP VARIANTS AS, AND VARIANTS ASP-430; SER-444; SER-619; ASN-664 AND
RP MET-1428.
RX MEDLINE=97094179; PubMed=8940267;
RA Knebelmann B., Breillat C., Forestier L., Arrondel C., Jacassier D.,
RA Giatras I., Drouot L., Deschenes G., Gruenfeld J.-P., Broyer M.,
RA Gubler M.-C., Antignac C.;
RT "Spectrum of mutations in the COL4A5 collagen gene in X-linked Alport
RT syndrome.";
RL Am. J. Hum. Genet. 59:1221-1232(1996).
RN [18]
RP VARIANT AS ASP-1498.
RX MEDLINE=96233932; PubMed=8829632;
RA Tverskaya S., Bobrynina V., Tsalykova F., Ignatova M.,
RA Krasnopolskaya X., Evgrafov O.;
RT "Substitution of A1498D in noncollagen domain of a5(IV) collagen
RT chain associated with adult-onset X-linked Alport syndrome.";

```
RL   Hum. Mutat. 7:149-150(1996).
RN   [19]
RP   VARIANT AS GLN-1677.
RX   MEDLINE=97295089; PubMed=9150741;
RA   Barker D.F., Denison J.C., Atkin C.L., Gregory M.C.;
RT   "Common ancestry of three Ashkenazi-American families with Alport
RT   syndrome and COL4A5 R1677Q.";
RL   Hum. Genet. 99:681-684(1997).
RN   [20]
RP   VARIANTS AS ARG-174; ARG-177; ARG-325; CYS-1410; TRP-1421; THR-1517
RP   AND ASP-1596.
RX   MEDLINE=98112435; PubMed=9452056;
RA   Neri T.M., Zanelli P., de Palma G., Savi M., Rossetti S., Turco A.E.,
RA   Pignatti G.F., Galli L., Bruttini M., Renieri A., Mingarelli R.,
RA   Trivelli A., Pinciaroli A.R., Ragaiolo M., Rizzoni G.F., de Marchi M.;
RT   "Missense mutations in the COL4A5 gene in patients with X-linked
RT   Alport syndrome.";
RL   Hum. Mutat. Suppl. 1:S106-S109(1998).
RN   [21]
RP   VARIANTS AS VAL-420; 456-PRO--PRO-458 DEL; ASP-573; ASP-624; ASP-635;
RP   802-GLY--PRO-807 DEL; ARG-869; CYS-941; SER-1030; SER-1066; ASP-1143;
RP   ARG-1196; GLU-1261; SER-1357 AND ARG-1649.
RX   MEDLINE=99063529; PubMed=9848783;
RA   Martin P., Heiskari N., Zhou J., Leinonen A., Tumelius T., Hertz J.M.,
RA   Barker D.F., Gregory M.C., Atkin C.L., Styrkarsdottir U., Neumann H.,
RA   Springate J., Shows T.B., Pettersson E., Tryggvason K.;
RT   "High mutation detection rate in the COL4A5 collagen gene in suspected
RT   Alport syndrome using PCR and direct DNA sequencing.";
RL   J. Am. Soc. Nephrol. 9:2291-2301(1998).
RN   [22]
RP   VARIANTS AS GLU-579; LYS-633; ASP-947; VAL-953; ARG-1107; ARG-1158;
RP   SER-1170 AND TRP-1678, AND VARIANTS SER-444 AND ALA-739.
RX   MEDLINE=20030197; PubMed=10561141;
RA   Inoue Y., Nishio H., Shirakawa T., Nakanishi K., Nakamura H.,
RA   Sumino K., Nishiyama K., Iijima K., Yoshikawa N.;
RT   "Detection of mutations in the COL4A5 gene in over 90% of male
RT   patients with X-linked Alport's syndrome by RT-PCR and direct
RT   sequencing.";
RL   Am. J. Kidney Dis. 34:854-862(1999).
RN   [23]
RP   VARIANT AS ARG-822.

  Query Match             8.9%;  Score 116;  DB 1;  Length 1685;
  Best Local Similarity   35.1%;  Pred. No. 0.027;
  Matches   33;  Conservative    6;  Mismatches   37;  Indels   18;  Gaps    3;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIP-----KGKQKAQLRQREVVDLYNGMCLQ 57
              ||||   |            || |     :|     || :|    |  :  |      |
Db       1256 PQGPPGRP------------GLPGPEGPPGPLPGNGGIKG-EKGNPGQPGLPGLPGLKGDQ 1302

Qy         58 GPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              || |: |  .| || | : | ||:||  || | ||
Db       1303 GPPGLQGNPGRPGLNGMKGDPGLPGVPGFPGMKG 1336


RESULT 6
CQT7_HUMAN
ID   CQT7_HUMAN     STANDARD;      PRT;   289 AA.
AC   Q9BXJ2;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Complement-c1q tumor necrosis factor-related protein 7 precursor.
GN   C1QTNF7 OR CTRP7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;
RT   "Homo sapiens complement-c1q tumor necrosis factor-related protein.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SIMILARITY: Contains 1 collagenous domain.
CC   -!- SIMILARITY: Contains 1 C1Q domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF329839; AAK17963.1; -.
DR   EMBL; BC022187; AAH22187.1; -.
DR   Genew; HGNC:14342; C1QTNF7.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 2.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Collagen; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    289       COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
FT                                 RELATED PROTEIN 7.
FT   DOMAIN       38    139       COLLAGEN-LIKE.
FT   DOMAIN      141    276       C1Q.
SQ   SEQUENCE   289 AA;  30683 MW;  A61609FF86D26946 CRC64;

  Query Match             8.9%;  Score 115.5;  DB 1;  Length 289;
  Best Local Similarity   46.3%;  Pred. No. 0.0037;
  Matches   31;  Conservative    5;  Mismatches   22;  Indels    9;  Gaps    3;

Qy         30 ASEIPKGKQKAQLRQREVVDLYNGMC----LQGPAGVPGRDGSPGANVIPGTPGIPGRDG 85
              ||  |:|    ||:       |  :|    | || | || :|||| :   | ||  ||||
Db         14 ASGQPRGN---QLKGENYSPRY--ICSIPGLPGPPGPPGANGSPGPHGRIGLPGRDGRDG 68

Qy         86 FKGEKGE 92
              ||||||
Db         69 RKGEKGE 75


RESULT 7
CA1H_HUMAN
ID   CA1H_HUMAN     STANDARD;      PRT;  1516 AA.
AC   P39060; Q9UK38; Q9Y6Q7; Q9Y6Q8;
DT   01-FEB-1995 (Rel. 31, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
```

```
DE   Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin].
GN   COL18A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98164096; PubMed=9503365;
RA   Saarela J., Ylikarppa R., Rehn M., Purmonen S., Pihlajaniemi T.;
RT   "Complete primary structure of two variant forms of human type XVIII
RT   collagen and tissue-specific differences in the expression of the
RT   corresponding transcripts.";
RL   Matrix Biol. 16:319-328(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20289799; PubMed=10830953;
RA   Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA   Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA   Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA   Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA   Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA   Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA   Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA   Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA   Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA   Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA   Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA   Lehrach H., Reinhardt R., Yaspo M.-L.;
RT   "The DNA sequence of human chromosome 21.";
RL   Nature 405:311-319(2000).
RN   [3]
RP   SEQUENCE OF 834-1516 FROM N.A.
RX   MEDLINE=94245237; PubMed=8188291;
RA   Oh S.P., Warman M.L., Seldin M.F., Cheng S., Knoll J.H., Timmons S.,
RA   Olsen B.R.;
RT   "Cloning of cDNA and genomic DNA encoding human type XVIII collagen
RT   and localization of the alpha 1(XVIII) collagen gene to mouse
RT   chromosome 10 and human chromosome 21.";
RL   Genomics 19:494-499(1994).
RN   [4]
RP   SEQUENCE OF 1334-1516 FROM N.A.
RC   TISSUE=Placenta;
RA   Zhi-Yong H., Biao L., Wei-Jie Z., Xiang-Fu W.;
RT   "Cloning and expression of human endostatin gene in Escherichia
RT   coli.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   INVOLVEMENT IN KNOBLOCH SYNDROME.
RX   MEDLINE=20400145; PubMed=10942434;
RA   Sertie A.L., Sossi V., Camargo A.A., Zatz M., Brahe C.,
RA   Passos-Bueno M.R.;
RT   "Collagen XVIII, containing an endogenous inhibitor of angiogenesis
RT   and tumor growth, plays a critical role in the maintenance of retinal
RT   structure and in neural tube closure.";
RL   Hum. Mol. Genet. 9:2051-2058(2000).
RN   [6]
RP   VARIANT ASN-1437.
RX   MEDLINE=21518361; PubMed=11606364;
RA   Iughetti P., Suzuki O., Godoi P.H., Alves V.A., Sertie A.L.,
RA   Zorick T., Soares F., Camargo A., Moreira E.S., di Loreto C.,
RA   Moreira-Filho C.A., Simpson A., Oliva G., Passos-Bueno M.R.;
RT   "A polymorphism in endostatin, an angiogenesis inhibitor, predisposes
RT   for the development of prostatic adenocarcinoma.";
RL   Cancer Res. 61:7375-7378(2001).
CC   -!- FUNCTION: COLA18A PROBABLY PLAYS A MAJOR ROLE IN DETERMINING THE
CC       RETINAL STRUCTURE AS WELL AS IN THE CLOSURE OF THE NEURAL TUBE.
CC   -!- FUNCTION: ENDOSTATIN POTENTLY INHIBITS ENDOTHELIAL CELL
CC       PROLIFERATION AND ANGIOGENESIS. MAY INHIBIT ANGIOGENESIS BY
CC       BINDING TO THE HEPARAN SULPHATE PROTEOGLYCANS INVOLVED IN GROWTH
CC       FACTOR SIGNALLING.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long; Synonyms=NC-493;
CC         IsoId=P39060-1; Sequence=Displayed;
CC       Name=Short; Synonyms=NC1-303;
CC         IsoId=P39060-2; Sequence=VSP_001155, VSP_001156;
CC   -!- TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS
CC       IN LIVER, LUNG AND KIDNEY.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- POLYMORPHISM: There is an association between a polymorphism in
CC       position 1437 and prostate cancer. Heterozygous Asn-1437
CC       individuals have a 2.5 times increased chance of developing
CC       prostate cancer as compared with homozygous Asp-1437 individuals.
CC   -!- DISEASE: Defects in COL18A1 are a cause of Knobloch syndrome (KNO)
CC       [MIM:267750]; an autosomal recessive disorder defined by the
CC       occurrence of high myopia, vitreoretinal degeneration with retinal
CC       detachment, macular abnormalities and occipital encephalocele.
CC   -!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
CC       INTERRUPTED HELICES (FACIT) FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF018081; AAC39658.1; -.
DR   EMBL; AF018082; AAC39659.1; -.
DR   EMBL; AL163302; CAB90482.1; -.
DR   EMBL; L22548; AAA51864.1; -.
DR   EMBL; AF184060; AAF01310.1; ALT_INIT.
DR   PDB; 1BNL; 02-DEC-98.
DR   GlycoSuiteDB; P39060; -.
DR   Genew; HGNC:2195; COL18A1.
DR   MIM; 120328; -.
DR   MIM; 267750; -.
DR   GO; GO:0005581; C:collagen; TAS.
DR   GO; GO:0008181; F:tumor suppressor; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   GO; GO:0007048; P:oncogenesis; TAS.
DR   GO; GO:0007601; P:vision; TAS.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR003129; TSPN.
DR   Pfam; PF01391; Collagen; 7.
DR   Pfam; PF02210; TSPN; 1.
DR   ProDom; PD000007; Clg_helix; 1.
DR   SMART; SM00282; LamG; 1.
DR   SMART; SM00210; TSPN; 1.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Cell adhesion; Collagen; Glycoprotein; Signal; Alternative splicing;
KW   Polymorphism; 3D-structure.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24   1516       COLLAGEN ALPHA 1(XVIII) CHAIN.
FT   CHAIN      1334   1516       ENDOSTATIN.
FT   DOMAIN       24    516       NONHELICAL REGION 1 (NC1).
FT   DOMAIN      517    550       TRIPLE-HELICAL REGION 1 (COL1).
FT   DOMAIN      551    560       NONHELICAL REGION 2 (NC2).
FT   DOMAIN      561    640       TRIPLE-HELICAL REGION 2 (COL2).
FT   DOMAIN      641    664       NONHELICAL REGION 3 (NC3).
FT   DOMAIN      665    786       TRIPLE-HELICAL REGION 3 (COL3).
FT   DOMAIN      787    809       NONHELICAL REGION 4 (NC4).
FT   DOMAIN      810    892       TRIPLE-HELICAL REGION 4 (COL4).
FT   DOMAIN      893    906       NONHELICAL REGION 5 (NC5).
FT   DOMAIN      907    948       TRIPLE-HELICAL REGION 5 (COL5).
FT   DOMAIN      949    961       NONHELICAL REGION 6 (NC6).
FT   DOMAIN      962   1034       TRIPLE-HELICAL REGION 6 (COL6).
FT   DOMAIN     1035   1044       NONHELICAL REGION 7 (NC7).
FT   DOMAIN     1045   1077       TRIPLE-HELICAL REGION 7 (COL7).
FT   DOMAIN     1078   1089       NONHELICAL REGION 8 (NC8).
FT   DOMAIN     1090   1111       TRIPLE-HELICAL REGION 8 (COL8).
```

```
FT   DOMAIN      1112   1118       NONHELICAL REGION 9 (NC9).
FT   DOMAIN      1119   1173       TRIPLE-HELICAL REGION 9 (COL9).
FT   DOMAIN      1174   1186       NONHELICAL REGION 10 (NC10).
FT   DOMAIN      1187   1204       TRIPLE-HELICAL REGION 10 (COL10).
FT   DOMAIN      1205   1516       NONHELICAL REGION 11 (NC11).
FT   CARBOHYD      68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     691    691       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    1329   1329       O-LINKED (GALNAC. . .).
FT                                 /FTId=CAR_000150.
FT   DISULFID    1366   1506       BY SIMILARITY.
FT   DISULFID    1468   1498       BY SIMILARITY.
FT   SITE        1095   1097       CELL ATTACHMENT SITE (POTENTIAL).
FT   VARSPLIC       1    180       Missing (in isoform Short).
FT                                 /FTId=VSP_001155.
FT   VARSPLIC     181    215       HTTEAGTLPAPTPSPPSLGRPWAPLTGPSVPPPSS -> MA
FT                                 PRCPWPWPRRRRLLDVLAPLVLLLGVRAASAEP (in
FT                                 isoform Short).
FT                                 /FTId=VSP_001156.
FT   VARIANT     1437   1437       D -> N (increased risk of developing
FT                                 prostate cancer).
FT                                 /FTId=VAR_012709.
FT   CONFLICT     428    428       F -> S (IN REF. 2).
FT   CONFLICT     841    841       I -> V (IN REF. 2).
FT   CONFLICT     877    877       V -> L (IN REF. 3).
FT   CONFLICT     886    886       P -> R (IN REF. 3).
FT   CONFLICT     912    912       P -> R (IN REF. 3).
FT   CONFLICT     933    933       R -> L (IN REF. 3).
FT   CONFLICT     975    975       P -> L (IN REF. 3).
FT   CONFLICT    1064   1064       A -> P (IN REF. 3).
FT   CONFLICT    1084   1084       L -> K (IN REF. 3).
FT   CONFLICT    1120   1120       P -> A (IN REF. 3).
FT   CONFLICT    1123   1123       P -> A (IN REF. 3).
FT   CONFLICT    1126   1126       P -> PPGP (IN REF. 2).
FT   CONFLICT    1206   1206       G -> GQ (IN REF. 3).
FT   CONFLICT    1304   1304       R -> G (IN REF. 3).
FT   CONFLICT    1314   1314       A -> G (IN REF. 3).
FT   CONFLICT    1323   1324       LR -> CG (IN REF. 3).
FT   CONFLICT    1443   1443       R -> T (IN REF. 4).
FT   CONFLICT    1483   1483       S -> Y (IN REF. 4).
SQ   SEQUENCE   1516 AA;  153840 MW;  3C70F29A4476EE76 CRC64;

  Query Match             8.9%;  Score 115.5;  DB 1;  Length 1516;
  Best Local Similarity   44.1%;  Pred. No. 0.026;
  Matches   26;  Conservative    8;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         52 NGMCLQGPA---GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYK 107
              |   : |||   |||||:| ||   :|| || |||:|  |  |:  : |  |:  | :|
Db        691 NSSDVPGPAGLPGVPGREGPPGFPGLPGPPGPPGREGPPGRTGQ--KGSLGEAGAPGHK 747


RESULT 8
CA14_HUMAN
ID   CA14_HUMAN     STANDARD;      PRT;  1669 AA.
AC   P02462;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 1(IV) chain precursor.
GN   COL4A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89340433; PubMed=2701944;
RA   Soininen R., Huotari M., Ganguly A., Prockop D.J., Tryggvason K.;
RT   "Structural organization of the gene for the alpha 1 chain of human
RT   type IV collagen.";
RL   J. Biol. Chem. 264:13565-13571(1989).
RN   [2]
RP   SEQUENCE OF 46-1257 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=88083584; PubMed=3691802;
RA   Soininen R., Haka-Risku T., Prockop D.J., Tryggvason K.;
RT   "Complete primary structure of the alpha 1-chain of human basement
RT   membrane (type IV) collagen.";
RL   FEBS Lett. 225:188-194(1987).
RN   [3]
RP   SEQUENCE OF 1-943 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=88029471; PubMed=3311751;
RA   Brazel D., Oberbaeumer I., Dieringer H., Babel W., Glanville R.W.,
RA   Deutzmann R., Kuehn K.;
RT   "Completion of the amino acid sequence of the alpha 1 chain of human
RT   basement membrane collagen (type IV) reveals 21 non-triplet
RT   interruptions located within the collagenous domain.";
RL   Eur. J. Biochem. 168:529-536(1987).
RN   [4]
RP   SEQUENCE OF 28-243.
RX   MEDLINE=86004708; PubMed=4043082;
RA   Glanville R.W., Qian R.Q., Siebold B., Risteli J., Kuehn K.;
RT   "Amino acid sequence of the N-terminal aggregation and cross-linking
RT   region (7S domain) of the alpha 1 (IV) chain of human basement
RT   membrane collagen.";
RL   Eur. J. Biochem. 152:213-219(1985).
RN   [5]
RP   SEQUENCE OF 534-1447.
RX   MEDLINE=85003629; PubMed=6434307;
RA   Babel W., Glanville R.W.;
RT   "Structure of human-basement-membrane (type IV) collagen. Complete
RT   amino-acid sequence of a 914-residue-long pepsin fragment from the
RT   alpha 1(IV) chain.";
RL   Eur. J. Biochem. 143:545-556(1984).
RN   [6]
RP   SEQUENCE OF 1256-1669 FROM N.A.
RX   MEDLINE=85207819; PubMed=2581969;
RA   Pihlajaniemi T., Tryggvason K., Myers J.C., Kurkinen M., Lebo R.,
RA   Cheung M.-C., Prockop D.J., Boyd C.D.;
RT   "cDNA clones coding for the pro-alpha1(IV) chain of human type IV
RT   procollagen reveal an unusual homology of amino acid sequences in two
RT   halves of the carboxyl-terminal domain.";
RL   J. Biol. Chem. 260:7681-7687(1985).
RN   [7]
RP   SEQUENCE OF 1259-1669 FROM N.A.
RX   MEDLINE=85216555; PubMed=2582422;
RA   Brinker J.M., Gudas L.J., Loidl H.R., Wang S.-Y., Rosenbloom J.,
RA   Kefalides N.A., Myers J.C.;
RT   "Restricted homology between human alpha 1 type IV and other
RT   procollagen chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:3649-3653(1985).
RN   [8]
RP   SEQUENCE OF 1-28 FROM N.A.
RX   MEDLINE=89034231; PubMed=3182844;
RA   Soininen R., Huotari M., Hostikka S.L., Prockop D.J., Tryggvason K.;
RT   "The structural genes for alpha 1 and alpha 2 chains of human type IV
RT   collagen are divergently encoded on opposite DNA strands and have an
RT   overlapping promoter region.";
RL   J. Biol. Chem. 263:17217-17220(1988).
RN   [9]
RP   SEQUENCE OF 1441-1669, AND DISULFIDE BONDS.
RC   TISSUE=Placenta;
RX   MEDLINE=89005112; PubMed=2844531;
RA   Siebold B., Deutzmann R., Kuehn K.;
RT   "The arrangement of intra- and intermolecular disulfide bonds in the
RT   carboxyterminal, non-collagenous aggregation and cross-linking domain
RT   of basement-membrane type IV collagen.";
RL   Eur. J. Biochem. 176:617-624(1988).
CC   -!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF
CC       GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
CC       MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
CC       NIDOGEN.
CC   -!- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
CC       ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
```

```
CC       WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
CC   -!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
CC       DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
CC       G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CC       CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
CC       TRIPLE-HELICAL 7S DOMAIN.
CC   -!- PTM: Lysines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in all cases and bind carbohydrates.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- PTM: Type IV collagens contain numerous cysteine residues which
CC       are involved in inter- and intramolecular disulfide bonding. 12 of
CC       these, located in the NC1 domain, are conserved in all known type
CC       IV collagens.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M26576; AAA53098.1; -.
DR   EMBL; J04217; AAA53098.1; JOINED.
DR   EMBL; M26550; AAA53098.1; JOINED.
DR   EMBL; M26540; AAA53098.1; JOINED.
DR   EMBL; M26542; AAA53098.1; JOINED.
DR   EMBL; M26543; AAA53098.1; JOINED.
DR   EMBL; M26544; AAA53098.1; JOINED.
DR   EMBL; M26545; AAA53098.1; JOINED.
DR   EMBL; M26546; AAA53098.1; JOINED.
DR   EMBL; M26547; AAA53098.1; JOINED.
DR   EMBL; M26537; AAA53098.1; JOINED.
DR   EMBL; M26538; AAA53098.1; JOINED.
DR   EMBL; M26548; AAA53098.1; JOINED.
DR   EMBL; M26549; AAA53098.1; JOINED.
DR   EMBL; M26551; AAA53098.1; JOINED.
DR   EMBL; M26552; AAA53098.1; JOINED.
DR   EMBL; M26553; AAA53098.1; JOINED.
DR   EMBL; M26554; AAA53098.1; JOINED.
DR   EMBL; M26555; AAA53098.1; JOINED.
DR   EMBL; M26556; AAA53098.1; JOINED.
DR   EMBL; M26557; AAA53098.1; JOINED.
DR   EMBL; M26539; AAA53098.1; JOINED.
DR   EMBL; M26558; AAA53098.1; JOINED.
DR   EMBL; M26559; AAA53098.1; JOINED.
DR   EMBL; M26560; AAA53098.1; JOINED.
DR   EMBL; M26561; AAA53098.1; JOINED.
DR   EMBL; M26562; AAA53098.1; JOINED.
DR   EMBL; M26536; AAA53098.1; JOINED.
DR   EMBL; M26563; AAA53098.1; JOINED.
DR   EMBL; M26541; AAA53098.1; JOINED.
DR   EMBL; M26564; AAA53098.1; JOINED.
DR   EMBL; M26565; AAA53098.1; JOINED.
DR   EMBL; M26566; AAA53098.1; JOINED.
DR   EMBL; M26567; AAA53098.1; JOINED.
DR   EMBL; M26568; AAA53098.1; JOINED.
DR   EMBL; M26569; AAA53098.1; JOINED.
DR   EMBL; M26570; AAA53098.1; JOINED.
DR   EMBL; M26571; AAA53098.1; JOINED.
DR   EMBL; M26572; AAA53098.1; JOINED.
DR   EMBL; M26573; AAA53098.1; JOINED.
DR   EMBL; M26574; AAA53098.1; JOINED.
DR   EMBL; M26575; AAA53098.1; JOINED.
DR   EMBL; Y00706; CAA68698.1; -.
DR   EMBL; X05561; CAA29075.1; -.
DR   EMBL; M10940; AAA52006.1; -.
DR   EMBL; M11315; AAA52042.1; -.
DR   PIR; S16876; CGHU4B.
DR   Genew; HGNC:2202; COL4A1.
DR   MIM; 120130; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001442; ProcollagnC4.
DR   Pfam; PF01413; C4; 2.
DR   Pfam; PF01391; Collagen; 24.
DR   ProDom; PD000007; Clg_helix; 6.
DR   ProDom; PD003923; ProcollagnC4; 1.
DR   SMART; SM00111; C4; 2.
KW   Extracellular matrix; Connective tissue; Basement membrane;
KW   Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
FT   SIGNAL       1     27
FT   PROPEP      28    172       AMINO-TERMINAL PROPEPTIDE (7S DOMAIN).
FT   CHAIN      173   1669       COLLAGEN ALPHA 1(IV) CHAIN.
FT   DOMAIN     173   1440       TRIPLE-HELICAL REGION.
FT   DOMAIN    1441   1669       NONHELICAL REGION (NC1).
FT   CARBOHYD   126    126       N-LINKED (GLCNAC. . .).
FT   DISULFID  1460   1551       OR 1548.
FT   DISULFID  1493   1548       OR 1551.
FT   DISULFID  1505   1511
FT   DISULFID  1570   1665       OR 1662.
FT   DISULFID  1604   1662       OR 1665.
FT   DISULFID  1616   1622
FT   CONFLICT   237    238       SG -> KE (IN REF. 4).
FT   CONFLICT   241    241       G -> K (IN REF. 4).
FT   CONFLICT   319    319       Q -> A (IN REF. 3).
FT   CONFLICT   719    719       N -> D (IN REF. 5).
FT   CONFLICT   837    837       D -> Y (IN REF. 5).
FT   CONFLICT   842    842       K -> P (IN REF. 5).
FT   CONFLICT   896    896       V -> W (IN REF. 2).
FT   CONFLICT   904    904       E -> Q (IN REF. 5).
FT   CONFLICT   914    914       S -> K (IN REF. 5).
FT   CONFLICT   998    998       S -> K (IN REF. 5).
FT   CONFLICT  1010   1010       K -> P (IN REF. 5).
FT   CONFLICT  1012   1012       S -> K (IN REF. 5).
FT   CONFLICT  1358   1358       E -> Q (IN REF. 5).
SQ   SEQUENCE  1669 AA;  160611 MW;  3BEBA6DFFB9B8A84 CRC64;

  Query Match             8.9%;  Score 115.5;  DB 1;  Length 1669;
  Best Local Similarity   34.8%;  Pred. No. 0.029;
  Matches   32;  Conservative    5;  Mismatches   20;  Indels   35;  Gaps    4;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLP-APSSASEIPKGKQKAQLRQREVVDLYNGMCLQGP 59
              | | ||   |             || :|  |:| |||                     :||
Db       1212 MGPPGPQGQP-----------GLPGSPGHATEGPKGD-----------------RGP 1240

Qy         60 AGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
                | ||  | ||     | ||:|| || ||:||
Db       1241 QGQPGLPGLPGP---MGPPGLPGIDGVKGDKG 1269


RESULT 9
CA13_HUMAN
ID   CA13_HUMAN     STANDARD;      PRT;  1466 AA.
AC   P02461; Q15112;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 1(III) chain precursor.
GN   COL3A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin fibroblast;
RX   MEDLINE=89350838; PubMed=2764886;
RA   Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
RA   Prockop D.J.;
RT   "Structure of cDNA clones coding for the entire prepro alpha 1 (III)
RT   chain of human type III procollagen. Differences in protein structure
RT   from type I procollagen and conservation of codon preferences.";
RL   Biochem. J. 260:509-516(1989).
RN   [2]
RP   SEQUENCE OF 149-1225 FROM N.A.
```

RX MEDLINE=89386015; PubMed=2780304;
RA Janeczko R.A., Ramirez F.;
RT "Nucleotide and amino acid sequences of the entire human alpha 1
RT (III) collagen.";
RL Nucleic Acids Res. 17:6742-6742(1989).
RN [3]
RP SEQUENCE OF 168-398.
RX MEDLINE=77134724; PubMed=557335;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of cyanogen
RT bromide peptides from the amino-terminal segment of type III collagen
RT of human liver.";
RL Biochemistry 16:1158-1164(1977).
RN [4]
RP REVISIONS.
RA Seyer J.M.;
RL Submitted (DEC-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 399-727.
RX MEDLINE=79000343; PubMed=687591;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of five
RT consecutive CNBr peptides from type III collagen of human liver.";
RL Biochemistry 17:3404-3411(1978).
RN [6]
RP SEQUENCE OF 728-964.
RX MEDLINE=80198282; PubMed=6246925;
RA Seyer J.M., Mainardi C., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha 1
RT (III)-CB5 from type III collagen of human liver.";
RL Biochemistry 19:1583-1589(1980).
RN [7]
RP SEQUENCE OF 950-1466 FROM N.A.
RX MEDLINE=88189827; PubMed=3357782;
RA Mankoo B.S., Dalgleish R.;
RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";
RL Nucleic Acids Res. 16:2337-2337(1988).
RN [8]
RP REVISION TO 1184.
RX MEDLINE=89098346; PubMed=3211760;
RA Molyneux K., Dalgleish R.;
RT "Human type III collagen 'variant' is a cDNA cloning artefact.";
RL Nucleic Acids Res. 16:11833-11833(1988).
RN [9]
RP SEQUENCE OF 1065-1466 FROM N.A.
RX MEDLINE=85087944; PubMed=6096827;
RA Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,
RA Rosenbloom J., Myers J.C.;
RT "Molecular cloning and carboxyl-propeptide analysis of human type III
RT procollagen.";
RL Nucleic Acids Res. 12:9383-9394(1984).
RN [10]
RP SEQUENCE OF 965-1200.
RX MEDLINE=81208139; PubMed=7016180;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha
RT 1(III)-CB9 from type III collagen of human liver.";
RL Biochemistry 20:2621-2627(1981).
RN [11]
RP SEQUENCE OF 1176-1466 FROM N.A.
RX MEDLINE=85157600; PubMed=2579949;
RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1
RT (III) collagen. Partial characterization of the 3' end region of the
RT gene.";
RL J. Biol. Chem. 260:4357-4363(1985).
RN [12]
RP SEQUENCE OF 1161-1200 FROM N.A.
RX MEDLINE=86187804; PubMed=3754462;
RA Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I.,
RA Tolstoshev P., Brantly M., Crystal R.G.;
RT "Human type III collagen gene expression is coordinately modulated
RT with the type I collagen genes during fibroblast growth.";
RL Biochemistry 25:1408-1413(1986).
RN [13]
RP SEQUENCE OF 1-170 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88303360; PubMed=3405773;
RA Toman D., Ricca G., de Crombrugghe B.;
RT "Nucleotide sequence of a cDNA coding for the amino-terminal region
RT of human prepro alpha 1(III) collagen.";
RL Nucleic Acids Res. 16:7201-7201(1988).
RN [14]
RP SEQUENCE OF 1-176 FROM N.A.
RX MEDLINE=89378752; PubMed=2777083;
RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
RT "Cloning and analysis of the 5' portion of the human type-III
RT procollagen gene (COL3A1).";
RL Gene 78:255-265(1989).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=9101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [16]
RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.
RX MEDLINE=93293988; PubMed=8514866;
RA Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
RA Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
RA Cole C.W., Jaakkola P., Ryynaenen M., Pearce W.H., Yao J.S.T.,
RA Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
RA Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;
RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations
RT in the triple-helical domain of type III procollagen are an
RT infrequent cause of aortic aneurysms.";
RL J. Clin. Invest. 91:2539-2545(1993).
RN [17]
RP VARIANT THR-698.
RX MEDLINE=91045136; PubMed=2235526;
RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,
RA Wu Y., Ganguly A., Prockop D.J.;
RT "G to A polymorphism in exon 31 of the COL3A1 gene.";
RL Nucleic Acids Res. 18:6180-6180(1990).
RN [18]
RP VARIANT AORTIC ANEURYSM ARG-786.
RX MEDLINE=91056145; PubMed=2243125;
RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
RT "A mutation in the gene for type III procollagen (COL3A1) in a family
RT with aortic aneurysms.";
RL J. Clin. Invest. 86:1465-1473(1990).
RN [19]
RP VARIANT EDS-IV ARG-828.
RX MEDLINE=94016385; PubMed=8411057;
RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
RT "The substitution of glycine 661 by arginine in type III collagen
RT produces mutant molecules with different thermal stabilities and
RT causes Ehlers-Danlos syndrome type IV.";
RL J. Med. Genet. 30:690-693(1993).
RN [20]
RP VARIANT EDS-IV SER-957.
RX MEDLINE=89109135; PubMed=2492273;
RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
RT "A single base mutation that substitutes serine for glycine 790 of
RT the alpha 1 (III) chain of type III procollagen exposes an arginine
RT and causes Ehlers-Danlos syndrome IV.";
RL J. Biol. Chem. 264:1349-1352(1989).
RN [21]
RP VARIANT EDS-IV VAL-960.
RX MEDLINE=95268429; PubMed=7749417;
RA Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi H.;
RT "Substitution of valine for glycine 793 in type III procollagen in
RT Ehlers-Danlos syndrome type IV.";
RL Hum. Mutat. 5:179-181(1995).

```
RN   [22]
RP   VARIANT EDS-IV GLU-1014.
RX   MEDLINE=92316511; PubMed=1352273;
RA   Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
RA   Pope F.M.;
RT   "A single base mutation in the gene for type III collagen (COL3A1)
RT   converts glycine 847 to glutamic acid in a family with Ehlers-Danlos
RT   syndrome type IV. An unaffected family member is mosaic for the
RT   mutation.";
RL   Hum. Genet. 89:414-418(1992).
RN   [23]
RP   VARIANT EDS-IV ASP-1050.
RX   MEDLINE=90037070; PubMed=2808425;
RA   Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
RT   "Single base mutation in the type III procollagen gene that converts
RT   the codon for glycine 883 to aspartate in a mild variant of
RT   Ehlers-Danlos syndrome IV.";
RL   J. Biol. Chem. 264:19313-19317(1989).
RN   [24]
RP   VARIANT EDS-IV VAL-1077.
RX   MEDLINE=91374480; PubMed=1895316;
RA   Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
RA   Pope F.M.;
RT   "Characterisation of a glycine to valine substitution at amino acid
RT   position 910 of the triple helical region of type III collagen in a
RT   patient with Ehlers-Danlos syndrome type IV.";
RL   J. Med. Genet. 28:458-463(1991).
RN   [25]
RP   VARIANT EDS-IV GLU-1173.
RX   MEDLINE=93022543; PubMed=1357232;
RA   Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
```

```
  Query Match             8.8%;  Score 115;  DB 1;  Length 1466;
  Best Local Similarity   36.1%;  Pred. No. 0.028;
  Matches   39;  Conservative    8;  Mismatches   47;  Indels   14;  Gaps    5;

Qy         22 LQLPAPSSASEIPKGKQKAQLRQREVVDLY--NGMCLQGPAGVPGRDGSPGANVIPGTPG 79
              |  | |    ||| |:  |   |          ||   ||| | ||  | || |  || ||
Db         72 LDCPNP----EIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPG 127

Qy         80 IPGRDGFKGEKGECLRESF---EESWTPNYKQCSWSSLNYGIDLGKIA 124
                 ||  |  |  | |  ||     ::::| |       |   |: :| :|
Db        128 QPGSPGSPGPPGIC--ESCPTGPQNYSPQYDSYDVKS---GVAVGGLA 170
```

```
RESULT 10
CA24_ASCSU
ID   CA24_ASCSU     STANDARD;      PRT;  1763 AA.
AC   P27393;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 2(IV) chain precursor.
OS   Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC   Ascarididae; Ascaris.
OX   NCBI_TaxID=6253;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS I AND II).
RX   MEDLINE=91340768; PubMed=1714907;
RA   Pettitt J., Kingston I.B.;
RT   "The complete primary structure of a nematode alpha 2(IV) collagen
RT   and the partial structural organization of its gene.";
RL   J. Biol. Chem. 266:16149-16156(1991).
CC   -!- FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES.
CC   -!- SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN.
CC       TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
CC       INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND BETWEEN NC1
CC       DOMAINS.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=I;
CC         IsoId=P27393-1; Sequence=Displayed;
CC       Name=II;
CC         IsoId=P27393-2; Sequence=VSP_001159;
CC   -!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
CC       DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
CC       G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CC       CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
CC       TRIPLE-HELICAL 7S DOMAIN.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- PTM: Type IV collagens contain numerous cysteine residues which
CC       are involved in inter- and intramolecular disulfide bonding. 12 of
CC       these, located in the NC1 domain, are conserved in all known type
CC       IV collagens.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M67507; AAA18014.1; -.
DR   PIR; S16366; S16366.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001442; ProcollagnC4.
DR   Pfam; PF01413; C4; 2.
DR   Pfam; PF01391; Collagen; 25.
DR   ProDom; PD000007; Clg_helix; 6.
DR   ProDom; PD003923; ProcollagnC4; 1.
DR   SMART; SM00111; C4; 2.
KW   Hydroxylation; Connective tissue; Basement membrane; Repeat; Collagen;
KW   Alternative splicing; Glycoprotein; Signal.
FT   SIGNAL       1     26       POTENTIAL.
FT   CHAIN       27   1763       COLLAGEN ALPHA 2(IV) CHAIN.
FT   DOMAIN      27     42       7S DOMAIN.
FT   DOMAIN      43   1529       TRIPLE-HELICAL REGION.
FT   DOMAIN    1530   1763       NONHELICAL REGION (NC1).
FT   DISULFID  1548   1637       OR 1634 (BY SIMILARITY).
FT   DISULFID  1581   1634       OR 1637 (BY SIMILARITY).
FT   DISULFID  1593   1599       BY SIMILARITY.
FT   DISULFID  1656   1752       OR 1749 (BY SIMILARITY).
FT   DISULFID  1690   1749       OR 1752 (BY SIMILARITY).
FT   DISULFID  1702   1709       BY SIMILARITY.
FT   CARBOHYD   126    126       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   249    249       O-LINKED (XYL. . .) (GLYCOSAMINOGLYCAN)
FT                               (IN ISOFORM II) (POTENTIAL).
FT   VARSPLIC   230    266       GEQGPRGPQGPPGPVPSTGAKGTIIGPEGAPGMKGEK ->
FT                               GDIGPAGPPGPPGPREFTGSGSIVGPRGHSGDKGVK (in
FT                               isoform II).
FT                               /FTId=VSP_001159.
SQ   SEQUENCE   1763 AA;  168526 MW;  304F528BC06AAE0D CRC64;
```

```
  Query Match             8.8%;  Score 115;  DB 1;  Length 1763;
  Best Local Similarity   25.4%;  Pred. No. 0.034;
  Matches   66;  Conservative   24;  Mismatches   94;  Indels   76;  Gaps   16;

Qy          5 GPAASPQRLRGLLLLLLLQ-LPAPSSASEIPKGKQKAQLRQREVVDLYNGM-CLQGPAGV 62
              ||  :|  :||   |  |  || ||     | |   |: |    | : |   : |  |
Db       1449 GPMGAP-GIRGEKGLPGLDGLPGPSG----PPGFAGAKGR-----DGFPGQPGMPGEKGA 1498

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESF---EESWTPNYKQCS------W-- 111
              ||  | ||   ||| ||:||  |  |  |   :: |   : | |    ||       |
Db       1499 PGLPGFPGIEGIPGPPGLPGPSGPPGPPGPSYKDGFLLVKHSQTSEVPQCPPGMVKLWDG 1558

Qy        112 --------SSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNAC-------CQR 156
                     :  ::  |||    |    :   | :  ||         | |
Db       1559 YSLLYIEGNEKSHNQDLGHAGSC----LSRFSTMPFLF-----CDVNNVCNYASRNDKSY 1609

Qy        157 WYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDV---AI 213
              |  |      : |:|:  :                |   |   |   :||   | :: |    |
Db       1610 WLST------TAPIPMMPV-----------SEGGIEPYISRCAVCEA-PANVIAVHSQTI 1651
```

```
Qy        214 WVGTCSDYPKGDASTGWNSV 233
              :  | :        ||||:
Db       1652 QIPNCPN--------GWNSL 1663


RESULT 11
CA64_HUMAN
ID   CA64_HUMAN     STANDARD;      PRT;  1691 AA.
AC   Q14031; Q12823; Q14053; Q9NQM5; Q9NTX3; Q9UJ76; Q9UMG6; Q9Y4L4;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 6(IV) chain precursor.
GN   COL4A6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM B).
RC   TISSUE=Eye, and Kidney;
RX   MEDLINE=94171779; PubMed=8125972;
RA   Oohashi T., Sugimoto M., Mattei M.-G., Ninomiya Y.;
RT   "Identification of a new collagen IV chain, alpha 6(IV), by cDNA
RT   isolation and assignment of the gene to chromosome Xq22, which is the
RT   same locus for COL4A5.";
RL   J. Biol. Chem. 269:7520-7526(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RX   MEDLINE=94230418; PubMed=8175748;
RA   Zhou J., Ding M., Zhao Z., Reeders S.T.;
RT   "Complete primary structure of the sixth chain of human basement
RT   membrane collagen, alpha 6(IV). Isolation of the cDNAs for alpha 6(IV)
RT   and comparison with five other type IV collagen chains.";
RL   J. Biol. Chem. 269:13193-13199(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND B), AND VARIANTS ALA-455 AND
RP   LYS-1110.
RX   MEDLINE=96299642; PubMed=8661006;
RA   Zhang X., Zhou J., Reeders S.T., Tryggvason K.;
RT   "Structure of the human type IV collagen COL4A6 gene, which is mutated
RT   in Alport syndrome-associated leiomyomatosis.";
RL   Genomics 33:473-479(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Bird C., Grafham D., Lawlor S., Wilson S.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1-542 FROM N.A. (ISOFORM A).
RX   MEDLINE=93361972; PubMed=8356449;
RA   Zhou J., Mochizuki T., Smeets H., Antignac C., Laurila P.,
RA   de Paepe A., Tryggvason K., Reeders S.T.;
RT   "Deletion of the paired alpha 5(IV) and alpha 6(IV) collagen genes in
RT   inherited smooth muscle tumors.";
RL   Science 261:1167-1169(1993).
CC   -!- FUNCTION: Type IV collagen is the major structural component of
CC       glomerular basement membranes (GBM), forming a 'chicken-wire'
CC       meshwork together with laminins, proteoglycans and entactin/
CC       nidogen.
CC   -!- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
CC       ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH
CC       2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
CC   -!- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=Q14031-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=Q14031-2; Sequence=VSP_001174;
CC   -!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
CC       DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
CC       G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CC       CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
CC       TRIPLE-HELICAL 7S DOMAIN.
CC   -!- PTM: Prolines at the third position of the tripeptide repeating
CC       unit (G-X-Y) are hydroxylated in some or all of the chains.
CC   -!- PTM: Type IV collagens contain numerous cysteine residues which
CC       are involved in inter- and intramolecular disulfide bonding. 12 of
CC       these, located in the NC1 domain, are conserved in all known type
CC       IV collagens.
CC   -!- SIMILARITY: TO OTHER TYPE IV COLLAGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D21337; BAA04809.1; -.
DR   EMBL; U04845; AAA19569.2; -.
DR   EMBL; U47004; AAB19038.1; -.
DR   EMBL; U46959; AAB19038.1; JOINED.
DR   EMBL; U46961; AAB19038.1; JOINED.
DR   EMBL; U46962; AAB19038.1; JOINED.
DR   EMBL; U46963; AAB19038.1; JOINED.
DR   EMBL; U46964; AAB19038.1; JOINED.
DR   EMBL; U46965; AAB19038.1; JOINED.
DR   EMBL; U46966; AAB19038.1; JOINED.
DR   EMBL; U46967; AAB19038.1; JOINED.
DR   EMBL; U46968; AAB19038.1; JOINED.
DR   EMBL; U46969; AAB19038.1; JOINED.
DR   EMBL; U46970; AAB19038.1; JOINED.
DR   EMBL; U46971; AAB19038.1; JOINED.
DR   EMBL; U46972; AAB19038.1; JOINED.
DR   EMBL; U46973; AAB19038.1; JOINED.
DR   EMBL; U46974; AAB19038.1; JOINED.
DR   EMBL; U46975; AAB19038.1; JOINED.
DR   EMBL; U46976; AAB19038.1; JOINED.
DR   EMBL; U46977; AAB19038.1; JOINED.
DR   EMBL; U46978; AAB19038.1; JOINED.
DR   EMBL; U46979; AAB19038.1; JOINED.
DR   EMBL; U46980; AAB19038.1; JOINED.
DR   EMBL; U46981; AAB19038.1; JOINED.
DR   EMBL; U46982; AAB19038.1; JOINED.
DR   EMBL; U46983; AAB19038.1; JOINED.
DR   EMBL; U46984; AAB19038.1; JOINED.
DR   EMBL; U46985; AAB19038.1; JOINED.
DR   EMBL; U46986; AAB19038.1; JOINED.
DR   EMBL; U46987; AAB19038.1; JOINED.
DR   EMBL; U46988; AAB19038.1; JOINED.
DR   EMBL; U46989; AAB19038.1; JOINED.
DR   EMBL; U46990; AAB19038.1; JOINED.
DR   EMBL; U46991; AAB19038.1; JOINED.
DR   EMBL; U46992; AAB19038.1; JOINED.
DR   EMBL; U46993; AAB19038.1; JOINED.
DR   EMBL; U46994; AAB19038.1; JOINED.
DR   EMBL; U46995; AAB19038.1; JOINED.
DR   EMBL; U46996; AAB19038.1; JOINED.
DR   EMBL; U46997; AAB19038.1; JOINED.
DR   EMBL; U46998; AAB19038.1; JOINED.
DR   EMBL; U46999; AAB19038.1; JOINED.
DR   EMBL; U47000; AAB19038.1; JOINED.
DR   EMBL; U47001; AAB19038.1; JOINED.
DR   EMBL; U47002; AAB19038.1; JOINED.
DR   EMBL; U47003; AAB19038.1; JOINED.
DR   EMBL; U47004; AAB19039.1; -.
DR   EMBL; U46960; AAB19039.1; JOINED.
DR   EMBL; U46961; AAB19039.1; JOINED.
DR   EMBL; U46962; AAB19039.1; JOINED.
DR   EMBL; U46963; AAB19039.1; JOINED.
DR   EMBL; U46964; AAB19039.1; JOINED.
DR   EMBL; U46965; AAB19039.1; JOINED.
DR   EMBL; U46966; AAB19039.1; JOINED.
DR   EMBL; U46967; AAB19039.1; JOINED.
```

```
DR   EMBL; U46968; AAB19039.1; JOINED.
DR   EMBL; U46969; AAB19039.1; JOINED.
DR   EMBL; U46970; AAB19039.1; JOINED.
DR   EMBL; U46971; AAB19039.1; JOINED.
DR   EMBL; U46972; AAB19039.1; JOINED.
DR   EMBL; U46973; AAB19039.1; JOINED.
DR   EMBL; U46974; AAB19039.1; JOINED.
DR   EMBL; U46975; AAB19039.1; JOINED.
DR   EMBL; U46976; AAB19039.1; JOINED.
DR   EMBL; U46977; AAB19039.1; JOINED.
DR   EMBL; U46978; AAB19039.1; JOINED.
DR   EMBL; U46979; AAB19039.1; JOINED.
DR   EMBL; U46980; AAB19039.1; JOINED.
DR   EMBL; U46981; AAB19039.1; JOINED.
DR   EMBL; U46982; AAB19039.1; JOINED.
DR   EMBL; U46983; AAB19039.1; JOINED.
DR   EMBL; U46984; AAB19039.1; JOINED.
DR   EMBL; U46985; AAB19039.1; JOINED.
DR   EMBL; U46986; AAB19039.1; JOINED.
DR   EMBL; U46987; AAB19039.1; JOINED.
DR   EMBL; U46988; AAB19039.1; JOINED.
DR   EMBL; U46989; AAB19039.1; JOINED.
DR   EMBL; U46990; AAB19039.1; JOINED.
DR   EMBL; U46991; AAB19039.1; JOINED.
DR   EMBL; U46992; AAB19039.1; JOINED.
DR   EMBL; U46993; AAB19039.1; JOINED.
DR   EMBL; U46994; AAB19039.1; JOINED.
DR   EMBL; U46995; AAB19039.1; JOINED.
DR   EMBL; U46996; AAB19039.1; JOINED.
DR   EMBL; U46997; AAB19039.1; JOINED.
DR   EMBL; U46998; AAB19039.1; JOINED.
DR   EMBL; U46999; AAB19039.1; JOINED.
DR   EMBL; U47000; AAB19039.1; JOINED.
DR   EMBL; U47001; AAB19039.1; JOINED.
DR   EMBL; U47002; AAB19039.1; JOINED.
DR   EMBL; U47003; AAB19039.1; JOINED.
DR   EMBL; AL034369; CAA22265.1; -.
DR   EMBL; AL109943; CAB89263.1; -.
DR   EMBL; AL136080; CAB96748.1; -.
DR   EMBL; AL031177; CAA20120.1; -.
DR   EMBL; L22763; AAA16338.1; -.
DR   PIR; A54122; CGHU6B.
DR   Genew; HGNC:2208; COL4A6.
DR   MIM; 303631; -.
DR   GO; GO:0005587; C:collagen type IV; NAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR   GO; GO:0030198; P:extracellular matrix organization and bioge. . .; NAS.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001442; ProcollagnC4.
DR   Pfam; PF01413; C4; 2.
DR   Pfam; PF01391; Collagen; 20.
DR   ProDom; PD000007; Clg_helix; 4.
DR   ProDom; PD003923; ProcollagnC4; 1.
DR   SMART; SM00111; C4; 2.
KW   Extracellular matrix; Connective tissue; Basement membrane;
KW   Repeat; Hydroxylation; Glycoprotein; Cell adhesion; Collagen; Signal;
KW   Alternative splicing; Polymorphism.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23   1691       COLLAGEN ALPHA 6(IV) CHAIN.
FT   DOMAIN      23     46       7S DOMAIN.
FT   DOMAIN      47   1463       TRIPLE-HELICAL REGION.

  Query Match             8.7%;  Score 113.5;  DB 1;  Length 1691;
  Best Local Similarity   36.0%;  Pred. No. 0.045;
  Matches   36;  Conservative    9;  Mismatches   22;  Indels   33;  Gaps    7;

Qy          4 QGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGM--------- 54
              |||| :|    ||:  |      ||     ||||     :   ::    ||
Db        524 QGPAGAP----GLVGPL-----GPSG----PKGK-----KGEPILSTIQGMPGDRGDSGS 565

Qy         55 -CLQGPAGVPGRDGSPGANVIPGTPGIP--GRDGFKGEKG 91
               :|  | ||:|| ||   :|| ||:|  |  || ||||
Db        566 QGFRGVIGEPGKDGVPG---LPGLPGLPGDGGQGFPGEKG 602
```

```
RESULT 12
CA17_HUMAN
ID   CA17_HUMAN     STANDARD;      PRT;  2944 AA.
AC   Q02388; Q14054; Q16507;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
DE   collagen).
GN   COL7A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94327588; PubMed=8051117;
RA   Christiano A.M., Greenspan D.S., Lee S., Uitto J.;
RT   "Cloning of human type VII collagen. Complete primary sequence of the
RT   alpha 1(VII) chain and identification of intragenic polymorphisms.";
RL   J. Biol. Chem. 269:20256-20262(1994).
RN   [2]
RP   SEQUENCE OF 128-1493 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=93338437; PubMed=1307247;
RA   Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
RA   Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,
RA   Uitto J.;
RT   "The large non-collagenous domain (NC-1) of type VII collagen is
RT   amino-terminal and chimeric. Homology to cartilage matrix protein,
RT   the type III domains of fibronectin and the A domains of von
RT   Willebrand factor.";
RL   Hum. Mol. Genet. 1:475-481(1992).
RN   [3]
RP   SEQUENCE OF 815-1439 FROM N.A.
RX   MEDLINE=91334380; PubMed=1871109;
RA   Parente M.G., Chung L.C., Ryynaenen J., Woodley D.T., Wynn K.W.,
RA   Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.;
RT   "Human type VII collagen: cDNA cloning and chromosomal mapping of the
RT   gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:6931-6935(1991).
RN   [4]
RP   SEQUENCE OF 369-1255 FROM N.A.
RX   MEDLINE=93107742; PubMed=1469284;
RA   Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S.,
RA   Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III;
RT   "Noncollagenous (NC1) domain of collagen VII resembles multidomain
RT   adhesion proteins involved in tissue-specific organization of
RT   extracellular matrix.";
RL   J. Invest. Dermatol. 99:691-696(1992).
RN   [5]
RP   SEQUENCE OF 340-675 FROM N.A.
RC   TISSUE=Keratinocytes;
RX   MEDLINE=92231902; PubMed=1567409;
RA   Tanaka T., Takahashi K.,.Furukawa F., Imamura S.;
RT   "Molecular cloning and characterization of type VII collagen cDNA.";
RL   Biochem. Biophys. Res. Commun. 183:958-963(1992).
RN   [6]
RP   SEQUENCE OF 2395-2944 FROM N.A.
RX   MEDLINE=93271985; PubMed=8499916;
RA   Greenspan D.S.;
RT   "The carboxyl-terminal half of type VII collagen, including the non-
RT   collagenous NC-2 domain and intron/exon organization of the
RT   corresponding region of the COL7A1 gene.";
RL   Hum. Mol. Genet. 2:273-278(1993).
RN   [7]
RP   SEQUENCE OF 1-87 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=94375010; PubMed=8088784;
RA   Christiano A.M., Hoffman G.G., Chung-Honet L.C., Lee S., Cheng W.,
RA   Uitto J., Greenspan D.S.;
RT   "Structural organization of the human type VII collagen gene (COL7A1),
```

```
RT   composed of more exons than any previously characterized gene.";
RL   Genomics 21:169-179(1994).
RN   [8]
RP   REVIEW ON DEB VARIANTS.
RX   MEDLINE=98041696; PubMed=9375848;
RA   Jaervikallio A., Pulkkinen L., Uitto J.;
RT   "Molecular basis of dystrophic epidermolysis bullosa: mutations in
RT   the type VII collagen gene (COL7A1).";
RL   Hum. Mutat. 10:338-347(1997).
RN   [9]
RP   VARIANT DEB LYS-2798.
RX   MEDLINE=93291877; PubMed=8513326;
RA   Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
RA   Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;
RT   "A missense mutation in type VII collagen in two affected siblings
RT   with recessive dystrophic epidermolysis bullosa.";
RL   Nat. Genet. 4:62-66(1993).
RN   [10]
RP   VARIANT DEB SER-2040.
RX   MEDLINE=94224777; PubMed=8170945;
RA   Christiano A.M., Ryynaenen M., Uitto J.;
RT   "Dominant dystrophic epidermolysis bullosa: identification of a
RT   Gly-->Ser substitution in the triple-helical domain of type VII
RT   collagen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3549-3553(1994).
RN   [11]
RP   VARIANT DEB CYS-2623.
RX   MEDLINE=96081220; PubMed=8541842;
RA   Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto J.;
RT   "Pretibial epidermolysis bullosa: genetic linkage to COL7A1 and
RT   identification of a glycine-to-cysteine substitution in the triple-
RT   helical domain of type VII collagen.";
RL   Hum. Mol. Genet. 4:1579-1583(1995).
RN   [12]
RP   VARIANT DEB ARG-2043.
RX   MEDLINE=95164985; PubMed=7861014;
RA   Christiano A.M., Morricone A., Paradisi M., Angelo C., Mazzanti C.,
RA   Cavalieri R., Uitto J.;
RT   "A glycine-to-arginine substitution in the triple-helical domain of
RT   type VII collagen in a family with dominant dystrophic epidermolysis
RT   bullosa.";
RL   J. Invest. Dermatol. 104:438-440(1995).
RN   [13]
RP   VARIANTS DEB.
RX   MEDLINE=96220218; PubMed=8644729;
RA   Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
RT   "Glycine substitutions in the triple-helical region of type VII
RT   collagen result in a spectrum of dystrophic epidermolysis bullosa
RT   phenotypes and patterns of inheritance.";
RL   Am. J. Hum. Genet. 58:671-681(1996).
RN   [14]
RP   VARIANT DEB ARG-2575.
RX   MEDLINE=96154068; PubMed=8592061;
RA   Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J.;
RT   "Molecular basis of recessive dystrophic epidermolysis bullosa:
RT   genotype/phenotype correlation in a case of moderate clinical
RT   severity.";
RL   J. Invest. Dermatol. 106:119-124(1996).
RN   [15]
RP   VARIANT DEB ARG-1782.
RX   MEDLINE=96183562; PubMed=8618018;
RA   Christiano A.M., McGrath J.A., Uitto J.;
RT   "Influence of the second COL7A1 mutation in determining the
RT   phenotypic severity of recessive dystrophic epidermolysis bullosa.";
RL   J. Invest. Dermatol. 106:766-770(1996).
RN   [16]
RP   VARIANT DEB ASP-2073.
RX   MEDLINE=96310789; PubMed=8757758;
RA   Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M.,
RA   Uitto J., Pope F.M., Eady R.A.J.;
RT   "Clinicopathological correlations of compound heterozygous COL7A1
RT   mutations in recessive dystrophic epidermolysis bullosa.";
RL   J. Invest. Dermatol. 107:171-177(1996).
RN   [17]
RP   VARIANTS DEB TRP-1982; GLY-2008; ALA-2025; GLU-2049; TRP-2063 AND
RP   ARG-2575.
RX   MEDLINE=97465605; PubMed=9326325;
RA   Hovnanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost C.,
RA   Fraitag S., Christiano A.M., Uitto J., Lathrop M., Barrandon Y.,
RA   de Prost Y.;
RT   "Characterization of 18 new mutations in COL7A1 in recessive
RT   dystrophic epidermolysis bullosa provides evidence for distinct
RT   molecular mechanisms underlying defective anchoring fibril
RT   formation.";
RL   Am. J. Hum. Genet. 61:599-610(1997).
RN   [18]
RP   VARIANT DEB ARG-1652.
RX   MEDLINE=98106792; PubMed=9444387;
RA   Cserhalmi-Friedman P.B., Karpati S., Horvath A., Christiano A.M.;
RT   "Identification of a glycine substitution and a splice site mutation
RT   in the type VII collagen gene in a proband with mitis recessive
RT   dystrophic epidermolysis bullosa.";
RL   Arch. Dermatol. Res. 289:640-645(1997).
RN   [19]
RP   VARIANTS DEB ARG-2009 AND ARG-2043.
RX   MEDLINE=97358588; PubMed=9215684;
RA   Winberg J.-O., Hammami-Hauasli N., Nilssen O., Anton-Lamprecht I.,
RA   Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,
RA   Gedde-Dahl T. Jr., Bruckner-Tuderman L.;
RT   "Modulation of disease severity of dystrophic epidermolysis bullosa by
RT   a splice site mutation in combination with a missense mutation in the
RT   COL7A1 gene.";
RL   Hum. Mol. Genet. 6:1125-1135(1997).
RN   [20]
RP   VARIANTS DEB ASP-1519; ASP-2006; GLU-2015 AND ARG-2034.
RX   MEDLINE=98334662; PubMed=9668111;
RA   Hammami-Hauasli N., Schumann H., Raghunath M., Kilgus O., Luethi U.,
RA   Luger T., Bruckner-Tuderman L.;
RT   "Some, but not all, glycine substitution mutations in COL7A1 result in
RT   intracellular accumulation of collagen VII, loss of anchoring
RT   fibrils, and skin blistering.";
RL   J. Biol. Chem. 273:19228-19234(1998).
RN   [21]
RP   VARIANTS DEB CYS-2008; ARG-2207 AND SER-2775.
RX   MEDLINE=98410969; PubMed=9740253;
RA   Kon A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J.;
RT   "Novel COL7A1 mutations in dystrophic forms of epidermolysis
RT   bullosa.";
RL   J. Invest. Dermatol. 111:534-537(1998).
RN   [22]
RP   VARIANT DEB ARG-1347.
RX   MEDLINE=99019477; PubMed=9804332;
RA   Terracina M., Posteraro P., Schubert M., Sonego G., Atzori F.,
RA   Zambruno G., Bruckner-Tuderman L., Castiglia D.;
RT   "Compound heterozygosity for a recessive glycine substitution and a
RT   splice site mutation in the COL7A1 gene causes an unusually mild form
RT   of localized recessive dystrophic epidermolysis bullosa.";
RL   J. Invest. Dermatol. 111:744-750(1998).
RN   [23]
RP   VARIANTS DEB TRP-2034; VAL-2040; ARG-2043; ARG-2064 AND ASP-2713.
RX   MEDLINE=99072663; PubMed=9856843;

  Query Match             8.7%;  Score 113;  DB 1;  Length 2944;
  Best Local Similarity   33.7%;  Pred. No. 0.095;
  Matches   34;  Conservative    2;  Mismatches   23;  Indels   42;  Gaps    4;

Qy          3 PQGP------AASPQR-----LRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLY 51
              | ||      |  | |     |||        || ||    :|
Db       1792 PSGPNGAAGKAGDPGRDGLPGLRG-----EQGLPGPSGPPGLP---------------- 1829

Qy         52 NGMCLQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGE 92
                    | || || || |   | || || || ||||||:
Db       1830 ---------GKPGEDGKPGLNGKNGEPGDPGEDGRKGEKGD 1861


RESULT 13
```

```
C1QC_HUMAN
ID   C1QC_HUMAN     STANDARD;      PRT;   245 AA.
AC   P02747; Q96DL2; Q96H05;
DT   21-JUL-1986 (Rel. 01, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Complement C1q subcomponent, C chain precursor.
GN   C1QG OR C1QC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=91174759; PubMed=1706597;
RA   Sellar G.C., Blake D.J., Reid K.B.M.;
RT   "Characterization and organization of the genes encoding the A-, B-
RT   and C-chains of human complement subcomponent C1q. The complete
RT   derived amino acid sequence of human C1q.";
RL   Biochem. J. 274:481-490(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RA   Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 29-122.
RX   MEDLINE=80020137; PubMed=486087;
RA   Reid K.B.M.;
RT   "Complete amino acid sequences of the three collagen-like regions
RT   present in subcomponent C1q of the first component of human
RT   complement.";
RL   Biochem. J. 179:367-371(1979).
RN   [5]
RP   REVIEW OF C1Q DEFICIENCY.
RX   MEDLINE=98450587; PubMed=9777412;
RA   Petry F.;
RT   "Molecular basis of hereditary C1q deficiency.";
RL   Immunobiology 199:286-294(1998).
CC   -!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD
CC       C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
CC       COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT
CC       C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1
CC       TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
CC       FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
CC   -!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
CC       AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED
CC       OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
CC       A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF
CC       THE C CHAIN.
CC   -!- PTM: O-linked glycans consist of Glc-Gal disaccharides bound to
CC       the oxygen atom of post-translationally added hydroxyl groups.
CC   -!- DISEASE: Defects in C1QG are a cause of C1Q deficiency
CC       [MIM:120575]. It is a rare genetic disorder which is associated
CC       with recurrent infections and a high prevalence of lupus
CC       erythematosus-like symptoms. It is characterized by a loss of
CC       activation of the complement classical pathway.
CC   -!- SIMILARITY: Contains 1 collagenous domain.
CC   -!- SIMILARITY: Contains 1 C1Q domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK057792; BAB71575.1; -.
DR   EMBL; BC009016; AAH09016.1; -.
DR   PIR; S14351; C1HUQC.
DR   Genew; HGNC:1245; C1QG.
DR   MIM; 120575; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 1.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
KW   Repeat; Signal; Disease mutation.
FT   SIGNAL       1     28
FT   CHAIN       29    245       COMPLEMENT C1Q SUBCOMPONENT, C CHAIN.
FT   DOMAIN      31    112       COLLAGEN-LIKE.
FT   DOMAIN     113    245       C1Q.
FT   DISULFID    32     32       INTERCHAIN (WITH OTHER C CHAIN).
FT   MOD_RES     36     36       HYDROXYLATION.
FT   MOD_RES     39     39       HYDROXYLATION.
FT   MOD_RES     42     42       HYDROXYLATION.
FT   MOD_RES     45     45       HYDROXYLATION.
FT   MOD_RES     54     54       HYDROXYLATION.
FT   MOD_RES     57     57       HYDROXYLATION.
FT   MOD_RES     63     63       HYDROXYLATION.
FT   MOD_RES     66     66       HYDROXYLATION.
FT   MOD_RES     71     71       HYDROXYLATION.
FT   MOD_RES     75     75       HYDROXYLATION.
FT   CARBOHYD    75     75       O-LINKED (GAL. . .).
FT   MOD_RES     81     81       HYDROXYLATION.
FT   MOD_RES     84     84       HYDROXYLATION.
FT   CARBOHYD    84     84       O-LINKED (GAL. . .).
FT   MOD_RES     93     93       HYDROXYLATION.
FT   MOD_RES     96     96       HYDROXYLATION.
FT   MOD_RES     99     99       HYDROXYLATION.
FT   MOD_RES    105    105       HYDROXYLATION.
FT   VARIANT     43     43       G -> R (in C1Q deficiency).
FT                               /FTId=VAR_008542.
FT   CONFLICT    14     14       K -> R (IN REF. 2).
FT   CONFLICT    23     23       P -> A (IN REF. 1).
FT   CONFLICT    57     57       K -> P (IN REF. 4).
FT   CONFLICT    66     66       P -> K (IN REF. 4).
FT   CONFLICT    72     72       K -> P (IN REF. 4).
FT   CONFLICT    84     84       P -> K (IN REF. 4).
FT   CONFLICT    87     87       N -> D (IN REF. 4).
```

```
FT   CONFLICT     90     90       M -> N (IN REF. 4).
FT   CONFLICT    215    215       E -> G (IN REF. 2).
SQ   SEQUENCE   245 AA;  25774 MW;  FA17117EB7ABFC12 CRC64;

  Query Match             8.6%;  Score 112;  DB 1;  Length 245;
  Best Local Similarity   39.1%;  Pred. No. 0.0063;
  Matches   36;  Conservative    6;  Mismatches   28;  Indels   22;  Gaps    4;

Qy          5 GPAASPQRLRGL-LLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP 63
              ||:: |    || |||||| ||                || :     |    : |  | |
Db          4 GPSSLPH--LGLKLLLLLLLLP---------------LRGQANTGCYGIPGMPGLPGAP 45

Qy         64 GR---DGSPGANVIPGTPGIPGRDGFKGEKGE 92
              |:   || ||    || | |||  | ||:|||
Db         46 GKDGYDGLPGPKGEPGIPAIPGIRGPKGQKGE 77


RESULT 14
CA12_BOVIN
ID   CA12_BOVIN     STANDARD;      PRT;   747 AA.
AC   P02459; Q28070; Q9XT24;
DT   21-JUL-1986 (Rel. 01, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 1(II) chain precursor (Fragments).
GN   COL2A1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE OF 1-15.
RC   TISSUE=Cartilage;
RX   MEDLINE=73258693; PubMed=4732855;
RA   Miller E.J., Lunde L.G.;
RT   "Isolation and characterization of the cyanogen bromide peptides from
RT   the alpha 1(II) chain of bovine and human cartilage collagen.";
RL   Biochemistry 12:3153-3159(1973).
RN   [2]
RP   SEQUENCE OF 16-177.
RC   TISSUE=Cartilage;
RX   MEDLINE=76253504; PubMed=782511;
RA   Butler W.T., Miller E.J., Finch J.E. Jr.;
RT   "The covalent structure of cartilage collagen. Amino acid sequence of
RT   the NH2-terminal helical portion of the alpha 1 (II) chain.";
RL   Biochemistry 15:3000-3006(1976).
RN   [3]
RP   SEQUENCE OF 139-198.
RC   TISSUE=Cartilage;
RX   MEDLINE=77093864; PubMed=833147;
RA   Butler W.T., Finch J.E. Jr., Miller E.J.;
RT   "The covalent structure of cartilage collagen. Evidence for sequence
RT   heterogeneity of bovine alpha1(II) chains.";
RL   J. Biol. Chem. 252:639-643(1977).
RN   [4]
RP   SEQUENCE OF 139-417.
RC   TISSUE=Cartilage;
RX   MEDLINE=89231683; PubMed=2714276;
RA   Seyer J.M., Hasty K.A., Kang A.H.;
RT   "Covalent structure of collagen. Amino acid sequence of an
RT   arthritogenic cyanogen bromide peptide from type II collagen of
RT   bovine cartilage.";
RL   Eur. J. Biochem. 181:159-173(1989).
RN   [5]
RP   SEQUENCE OF 418-492.
RX   MEDLINE=74163168; PubMed=4857180;
RA   Butler W.T., Miller E.J., Finch J.E. Jr., Inagami T.;
RT   "Homologous regions of collagen alpha1(I) and alpha1(II) chains:
RT   apparent clustering of variable and invariant amino acid residues.";
RL   Biochem. Biophys. Res. Commun. 57:190-195(1974).
RN   [6]
RP   SEQUENCE OF 180-272 FROM N.A.
RC   TISSUE=Cartilage;
RX   MEDLINE=94194070; PubMed=7511638;
RA   Brand D.D., Myers L.K., Terato K., Whittington K.B., Stuart J.M.,
RA   Rosloniec E.F.;
RT   "Characterization of the T cell determinants in the induction of
RT   autoimmune arthritis by bovine alpha 1(II)-CB11 in H-2q mice.";
RL   J. Immunol. 152:3088-3097(1994).
RN   [7]
RP   SEQUENCE OF 417-566 FROM N.A.
RC   TISSUE=Cartilage;
RX   MEDLINE=99410731; PubMed=10479530;
RA   Tang B., Chiang T.M., Brand D.D., Gumanovskaya M.L., Stuart J.M.,
RA   Kang A.H., Myers L.K.;
RT   "Molecular definition and characterization of recombinant bovine CB8
RT   and CB10: immunogenicity and arthritogenicity.";
RL   Clin. Immunol. 92:256-264(1999).
RN   [8]
RP   SEQUENCE OF 567-747 FROM N.A.
RX   MEDLINE=85215651; PubMed=2582365;
RA   Sangiorgi F.O., Benson-Chanda V., de Wet W.J., Sobel M.E.,
RA   Ramirez F.;
RT   "Analysis of cDNA and genomic clones coding for the pro alpha 1 chain
RT   of calf type II collagen.";
RL   Nucleic Acids Res. 13:2815-2826(1985).
CC   -!- FUNCTION: COLLAGEN TYPE II IS SPECIFIC FOR CARTILAGINOUS TISSUES.
CC   -!- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(II) CHAINS.
CC   -!- PTM: Proline residues at the third position of the tripeptide
CC       repeating unit (G-X-Y) are hydroxylated in some or all of the
CC       chains. Hydroxylation on Pro-9 is involved in cross-linking.
CC   -!- PTM: O-linked glycans consist of Glc-Gal disaccharides bound to
CC       the oxygen atom of post-translationally added hydroxyl groups.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L28918; AAA30436.1; -.
DR   EMBL; AF138957; AAD42347.1; -.
DR   EMBL; X02420; CAA26269.1; -.
DR   PIR; A90369; CGBO6C.
DR   PIR; I45876; I45876.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   InterPro; IPR001007; VWF_C.
DR   ProDom; PD000007; Clg_helix; 2.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
DR   PROSITE; PS01208; VWFC_1; PARTIAL.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Glycoprotein; Cartilage; Collagen.
FT   CHAIN         1    >566       COLLAGEN ALPHA 1(II) CHAIN.
FT   NON_CONS    566     567
FT   PROPEP     <567     747       CARBOXYL-TERMINAL PROPEPTIDE.
FT   MOD_RES      9       9       HYDROXYLATION.
FT   MOD_RES    102     102       HYDROXYLATION.
FT   CARBOHYD   102     102       O-LINKED (GAL. . .).
FT   MOD_RES    114     114       HYDROXYLATION.
FT   CARBOHYD   114     114       O-LINKED (GAL. . .).
FT   MOD_RES    123     123       HYDROXYLATION.
FT   CARBOHYD   123     123       O-LINKED (GAL. . .).
FT   MOD_RES    189     189       HYDROXYLATION.
FT   MOD_RES    423     423       HYDROXYLATION.
FT   CARBOHYD   423     423       O-LINKED (GAL).
FT   MOD_RES    435     435       HYDROXYLATION.
FT   CARBOHYD   435     435       O-LINKED (GAL).
FT   VARIANT    143     143       L -> A (IN MINOR COMPONENT).
FT   VARIANT    164     164       Q -> L (IN MINOR COMPONENT).
FT   CONFLICT   179     179       G -> Z (IN REF. 3).
FT   CONFLICT   185     186       AP -> PA (IN REF. 3).
```

```
FT   CONFLICT    191    192       EA -> AS (IN REF. 3).
FT   CONFLICT    195    195       T -> Q (IN REF. 4).
FT   CONFLICT    215    215       S -> A (IN REF. 4).
FT   CONFLICT    227    227       T -> A (IN REF. 4).
FT   CONFLICT    251    251       P -> A (IN REF. 4).
FT   CONFLICT    258    258       Q -> T (IN REF. 4).
FT   CONFLICT    261    261       T -> S (IN REF. 4).
FT   CONFLICT    492    492       G -> P (IN REF. 5).
SQ   SEQUENCE   747 AA;  71329 MW;  D0FC1D7CD1CAF77C CRC64;

  Query Match             8.5%;  Score 111;  DB 1;  Length 747;
  Best Local Similarity   23.3%;  Pred. No. 0.029;
  Matches   47;  Conservative   19;  Mismatches   52;  Indels   84;  Gaps    8;

Qy         57 QGPAGVPGRDGSPGANVIP---GTPGIPGRDGFKGEKGE---------------------- 92
              :|  | ||  ||||| :    | || || || ||  |
Db        513 RGERGFPGERGSPGAQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMTLDAMK 572

Qy         93 --CLRESFEESWTPN----YKQCSWSS-------------------LNYGIDLGKIA--- 124
                |  |: |    ||     |:  |||                    :|| |   :|
Db        573 VFCNMETGETCVYPNPASVPKKNWWSSKSKDKKHIWFGETINGGFHFSYGDD--NLAPNT 630

Qy        125 ---ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQG 181
                 : || :: |       | ::   |:|                     :| |||:
Db        631 ADVQMTFLRLLSTEG-----SQNITYHCKN---------------------SIAYLDEA 663

Qy        182 SPEMNSTINIHRTSSVEGLCEG 203
              :  :   : |  :: ||   ||
Db        664 AGNLKKALLIQGSNDVEIRAEG 685


RESULT 15
CA11_RAT
ID   CA11_RAT       STANDARD;      PRT;   671 AA.
AC   P02454; P02455;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 1(I) chain (Fragments).
GN   COL1A1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE OF 1-19.
RX   MEDLINE=69155173; PubMed=5777344;
RA   Bornstein P.;
RT   "Comparative sequence studies of rat skin and tendon collagen. II.
RT   The absence of a short sequence at the amino terminus of the skin
RT   alpha-1 chain.";
RL   Biochemistry 8:63-71(1969).
RN   [2]
RP   SEQUENCE OF 5-19.
RX   MEDLINE=67162268; PubMed=5337886;
RA   Kang A.H., Bornstein P., Piez K.A.;
RT   "The amino acid sequence of peptides from the cross-linking region of
RT   rat skin collagen.";
RL   Biochemistry 6:788-795(1967).
RN   [3]
RP   SEQUENCE OF 20-55.
RX   MEDLINE=67165368; PubMed=4290711;
RA   Bornstein P.;
RT   "The incomplete hydroxylation of individual prolyl residues in
RT   collagen.";
RL   J. Biol. Chem. 242:2572-2574(1967).
RN   [4]
RP   SEQUENCE OF 56-102.
RX   MEDLINE=71263178; PubMed=4327399;
RA   Butler W.T., Ponds S.L.;
RT   "Chemical studies on the cyanogen bromide peptides of rat skin
RT   collagen. Amino acid sequence of alpha 1-CB4.";
RL   Biochemistry 10:2076-2081(1971).
RN   [5]
RP   SEQUENCE OF 103-139.
RX   MEDLINE=70085124; PubMed=5411206;
RA   Butler W.T.;
RT   "Chemical studies on the cyanogen bromide peptides of rat skin
RT   collagen. The covalent structure of alpha 1-CB5, the major
RT   hexose-containing cyanogen bromide peptide of alpha 1.";
RL   Biochemistry 9:44-50(1970).
RN   [6]
RP   SEQUENCE OF 140-238.
RX   MEDLINE=72136131; PubMed=4335087;
RA   Balian G., Click E.M., Bornstein P.;
RT   "Structure of rat skin collagen alpha 1-CB8. Amino acid sequence of
RT   the hydroxylamine-produced fragment HA1.";
RL   Biochemistry 10:4470-4478(1971).
RN   [7]
RP   SEQUENCE OF 239-418.
RX   MEDLINE=73006942; PubMed=4342027;
RA   Balian G., Click E.M., Hermodson M.A., Bornstein P.;
RT   "Structure of rat skin collagen alpha 1-CBB. Amino acid sequence of
RT   the hydroxyl amine-produced fragment HA2.";
RL   Biochemistry 11:3798-3806(1972).
RN   [8]
RP   SEQUENCE OF 419-567.
RX   MEDLINE=74271984; PubMed=4366532;
RA   Butler W.T., Underwood S.P., Finch J.E. Jr.;
RT   "Chemical studies on the cyanogen bromide peptides of rat skin
RT   collagen. Amino acid sequence of alpha 1-CB3.";
RL   Biochemistry 13:2946-2953(1974).
RN   [9]
RP   SEQUENCE OF 568-651.
RX   MEDLINE=74011954; PubMed=4126850;
RA   Stoltz M., Timpl R., Furthmayr H., Kuehn K.;
RT   "Structural and immunogenic properties of a major antigenic
RT   determinant in neutral salt-extracted rat-skin collagen.";
RL   Eur. J. Biochem. 37:287-294(1973).
RN   [10]
RP   SEQUENCE OF 651-671.
RX   MEDLINE=73049495; PubMed=4636751;
RA   Stoltz M., Timpl R., Kuehn K.;
RT   "Non-helical regions in rat collagen alpha 1-chain.";
RL   FEBS Lett. 26:61-65(1972).
RN   [11]
RP   SEQUENCE OF 529-567 FROM N.A.
RX   MEDLINE=85122694; PubMed=6395893;
RA   Genovese C., Rowe D., Kream B.;
RT   "Construction of DNA sequences complementary to rat alpha 1 and alpha
RT   2 collagen mRNA and their use in studying the regulation of type I
RT   collagen synthesis by 1,25-dihydroxyvitamin D.";
RL   Biochemistry 23:6210-6216(1984).
CC   -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
CC       (FIBRILLAR FORMING COLLAGEN).
CC   -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
CC   -!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
CC       BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
CC       HYDROXYAPATITE.
CC   -!- PTM: Proline residues at the third position of the tripeptide
CC       repeating unit (G-X-Y) are hydroxylated in some or all of the
CC       chains.
CC   -!- PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to
CC       the oxygen atom of a post-translationally added hydroxyl group.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M11432; AAA40832.1; ALT_SEQ.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001007; VWF_C.
```

```
DR   ProDom; PD000007; Clg_helix; 1.
DR   PROSITE; PS01208; VWFC_1; PARTIAL.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Glycoprotein; Collagen; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
FT   MOD_RES       9      9       CONVERTED TO AN ALDEHYDE GROUP THAT IS
FT                                 INVOLVED IN CROSS-LINKING.
FT   MOD_RES      28     28       HYDROXYLATION (PROBABLE).
FT   MOD_RES      31     31       HYDROXYLATION (PROBABLE).
FT   MOD_RES      34     34       HYDROXYLATION (PROBABLE).
FT   MOD_RES      43     43       HYDROXYLATION (PROBABLE).
FT   MOD_RES      46     46       HYDROXYLATION (PROBABLE).
FT   MOD_RES      49     49       HYDROXYLATION (PROBABLE).
FT   MOD_RES     103    103       HYDROXYLATION.
FT   CARBOHYD    103    103       O-LINKED (GAL. . .).
FT   MOD_RES     424    424       HYDROXYLATION (PROBABLE).
FT   MOD_RES     547    547       HYDROXYLATION (PROBABLE).
FT   NON_CONS    567    568
FT   DOMAIN      641    651       MAJOR ANTIGENIC DETERMINANT (OF NEUTRAL
FT                                 SALT-EXTRACTED RAT SKIN COLLAGEN).
SQ   SEQUENCE   671 AA;  60615 MW;  9DC3114204AC4918 CRC64;

  Query Match             8.5%;  Score 110.5;  DB 1;  Length 671;
  Best Local Similarity   35.2%;  Pred. No. 0.028;
  Matches   32;  Conservative    2;  Mismatches   24;  Indels   33;  Gaps    4;

Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||   |  || :||         | |      | |                   |||
Db        195 PQGARGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 223

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | || || |||    | ||| |  || | :|
Db        224 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 254


Search completed: August 13, 2003, 13:25:37
Job time : 25 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:22:37 ; Search time 39 Seconds
(without alignments)
599.205 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	122.5	9.4	246	2	S29328	complement subcomp
2	120	9.2	1752	2	A45407	collagen alpha 3(I
3	119	9.1	289	2	T20177	hypothetical prote
4	118.5	9.1	1464	1	CGHU1S	collagen alpha 1(I
5	117	9.0	327	2	T29031	hypothetical prote
6	117	9.0	754	2	A55267	collagen alpha 5(I
7	116	8.9	888	2	S28791	collagen alpha 1(X
8	116	8.9	1670	1	CGHU3B	collagen alpha 3(I
9	115.5	8.9	1669	1	CGHU4B	collagen alpha 1(I
10	115	8.8	1466	1	CGHU7L	collagen alpha 1(I
11	115	8.8	1763	2	S16366	collagen alpha 2(I
12	114.5	8.8	311	2	T15268	hypothetical prote
13	114	8.8	304	2	T26185	hypothetical prote
14	114	8.8	304	2	T26184	hypothetical prote
15	114	8.8	1691	1	S22917	collagen alpha 5(I
16	113.5	8.7	300	2	T24482	hypothetical prote
17	113.5	8.7	920	2	A45748	collagen alpha 1(V
18	113.5	8.7	1549	2	I48103	type VII collagen
19	113.5	8.7	1691	1	CGHU6B	collagen alpha 6(I
20	113	8.7	2944	2	A54849	collagen alpha 1(V
21	112	8.6	178	2	A39762	collagen alpha 1(X
22	112	8.6	325	2	T18594	hypothetical prote
23	111.5	8.6	428	2	T24769	hypothetical prote
24	111	8.5	245	1	C1HUQC	complement subcomp
25	111	8.5	358	2	T26281	hypothetical prote
26	110.5	8.5	298	2	T27644	hypothetical prote
27	110.5	8.5	310	2	T29731	hypothetical prote
28	110.5	8.5	458	2	T31631	hypothetical prote
29	110.5	8.5	671	1	CGRT1S	collagen alpha 1(I
30	110.5	8.5	1453	2	S21626	collagen alpha 1(I
31	110	8.5	298	2	JC1448	collagen col-34 -
32	110	8.5	299	2	T29956	hypothetical prote
33	110	8.5	1042	1	CGCH1S	collagen alpha 1(I
34	110	8.5	1049	1	CGBO7S	collagen alpha 1(I
35	110	8.5	1568	2	T09074	semaphorin recepto
36	110	8.5	1806	1	CGHU1E	collagen alpha 1(X
37	109.5	8.4	177	2	S37749	collagen alpha 2(X
38	109.5	8.4	290	2	T24586	hypothetical prote
39	109.5	8.4	330	2	S46657	collagen alpha 1(X
40	109.5	8.4	488	2	A27353	collagen alpha 1(I
41	109	8.4	1414	1	S23809	collagen alpha 2(I
42	109	8.4	1418	2	T45467	collagen alpha 1(I
43	109	8.4	1669	1	CGMS4B	collagen alpha 1(I
44	109	8.4	1744	2	S40991	collagen alpha 1(I
45	108.5	8.3	323	2	A61396	collagen alpha 1(I

ALIGNMENTS

RESULT 1
S29328
complement subcomponent C1q chain C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S29328
R;Petry, F.; Reid, K.B.M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
A;Title: Isolation, sequence analysis and characterization of cDNA clones coding for ecerebellin.
A;Reference number: S29328; MUID:93011118; PMID:1396691
A;Accession: S29328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <PET>
A;Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal
F;122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 9.4%; Score 122.5; DB 2; Length 246;
Best Local Similarity 37.4%; Pred. No. 0.0016;
Matches 34; Conservative 5; Mismatches 33; Indels 19; Gaps 2;

```
Qy          5 GPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
              ||:  ||    |||| || ||  | ||                |    : |  | ||
Db          4 GPSCQPQCGLCLLLLFLLALPLRSQAS----------------AGCYGIPGMPGMPGAPG 47

Qy         65 RDGS---PGANVIPGTPGIPGRDGFKGEKGE 92
                :||     |    || | :||  | ||:|||
Db         48 KDGHDGLQGPKGEPGIPAVPGTQGPKGQKGE 78
```

RESULT 2
A45407
collagen alpha 3(IV) chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A45407; A43903; A23940
R;Exposito, J.Y.; D'Alessio, M.; Di Liberto, M.; Ramirez, F.
J. Biol. Chem. 268, 5249-5254, 1993
A;Title: Complete primary structure of a sea urchin type IV collagen alpha chain and
A;Reference number: A45407; MUID:93186842; PMID:8444899
A;Accession: A45407
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1752 <EXP>
A;Note: sequence extracted from NCBI backbone (NCBIP:126841)
R;Wessel, G.M.; Etkin, M.; Benson, S.
Dev. Biol. 148, 261-272, 1991
A;Title: Primary mesenchyme cells of the sea urchin embryo require an autonomously pr
A;Reference number: A43903; MUID:92038439; PMID:1936564
A;Accession: A43903

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'P',633-1537,'G' <WES>
A;Cross-references: GB:S64572; NID:g238616; PIDN:AAB20270.1; PID:g238617
A;Note: sequence extracted from NCBI backbone (NCBIN:64572, NCBIP:64573)
R;Venkatesan, M.; De Pablo, F.; Vogeli, G.; Simpson, R.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 3351-3355, 1986
A;Title: Structure and developmentally regulated expression of a Strongylocentrotus purp
A;Reference number: A23940; MUID:86205894; PMID:3458186
A;Accession: A23940
A;Molecule type: DNA
A;Residues: 742-812 <VEN>
A;Cross-references: EMBL:M13206
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;29-161/Domain: amino-terminal nonhelical, 7S <7SD>
F;162-1523/Region: interrupted helical
F;1524-1752/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F;1534-1634/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1644-1748/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;129/Modified site: allysine (Lys) #status predicted

  Query Match             9.2%;  Score 120;  DB 2;  Length 1752;
  Best Local Similarity   22.4%;  Pred. No. 0.025;
  Matches   46;  Conservative   20;  Mismatches   61;  Indels   78;  Gaps    9;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV 62
              ||||     |           | |      | |                    | |  |
Db       1453 PQGPPGRDGR----------PGPQG----PPG------------------LTGDKGT 1477

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESF------------------EESWT 103
              ||  |:|| : :|| ||: |  ||:|: |:     |                  . | |
Db       1478 PGVQGNPGVSGVPGEPGLKGEQGFRGQNGQPGDPGFPGTKGEAGIPGSSSGFFITRHSQT 1537

Qy        104 PNYKQC------SW----------SSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRL 147
               :  ||      |          :   :| ||||   |    ::  | :  ||  ::
Db       1538 TSIPQCPQGTAKMWHGYSLLFVQGNERGHGQDLGKPGSC----LKRFSTMPFLFC-NINN 1592

Qy        148 KCRNACCQRWYFTFNGAECSGPLPI 172
               |  |   : :  :  |   |:|:
Db       1593 VCHVASRNDYSYWLSTTE---PMPM 1614


RESULT 3
T20177
hypothetical protein C53B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20177
R;Berks, M.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19233
A;Accession: T20177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-289 <WIL>
A;Cross-references: EMBL:Z68215; PIDN:CAA92453.1; GSPDB:GN00022; CESP:C53B4.5
A;Experimental source: clone C53B4
C;Genetics:
A;Gene: CESP:C53B4.5
A;Map position: 4
C;Superfamily: unassigned collagens

  Query Match             9.1%;  Score 119;  DB 2;  Length 289;
  Best Local Similarity   34.5%;  Pred. No. 0.004;
  Matches   29;  Conservative    5;  Mismatches   20;  Indels   30;  Gaps    2;

Qy         25 PAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGS--------------P 69
              | | |  |  :  |                  :|||| ||:||:           |
Db        203 PQPGSPGEPGRPGQPGS--------------RGPAGQPGKDGAQGGPGEKGANGEPGQP 247

Qy         70 GANVIPGTPGIPGRDGFKGEKGEC 93
              | :  || || |||||  |||| |


Db        248 GRDGQPGRPGQPGRDGHPGEKGVC 271


RESULT 4
CGHU1S
collagen alpha 1(I) chain precursor - human
N;Alternate names: procollagen alpha 1(I) chain
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 31-Dec-2000
C;Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567;
5269; A29439; I53466; A02852; I37247
R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P
Gene 67, 105-115, 1988
A;Title: Complete nucleotide sequence of the region encompassing the first twenty-fiv
A;Reference number: I60114; MUID:88329734; PMID:2843432
A;Accession: I60114
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369,'L',371-589 <DAL>
A;Cross-references: GB:M20789; NID:g179593; PIDN:AAB59373.1; PID:g179594
R;Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Pr
Biochem. J. 253, 919-922, 1988
A;Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of hum
A;Reference number: S01143; MUID:89025644; PMID:3178743
A;Accession: S01143
A;Molecule type: mRNA
A;Residues: 1-472 <TRO>
A;Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546;
A;Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988
R;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams,
Nature 310, 337-340, 1984
A;Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation
A;Reference number: A93335; MUID:84270697; PMID:6462220
A;Accession: A93335
A;Molecule type: DNA
A;Residues: 1-58,'Q',60-181 <CHU>
A;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658
R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet,
J. Biol. Chem. 262, 15151-15157, 1987
A;Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene
A;Reference number: I55254; MUID:88033098; PMID:2822714
A;Accession: I55254
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-45 <ROS>
A;Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388
R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional contro
A;Reference number: A39943; MUID:88097389; PMID:3480516
A;Accession: A39943
A;Molecule type: DNA
A;Residues: 1-34 <BOR>
A;Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238
R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promote
A;Reference number: I55237; MUID:85130970; PMID:2857713
A;Accession: I55237
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-34 <CH2>
A;Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226
R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holl
J. Biol. Chem. 265, 6312-6317, 1990
A;Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-term
rome, type VII.
A;Reference number: A35233; MUID:90202908; PMID:2318855
A;Accession: A35233
A;Molecule type: protein
A;Residues: 33-52 <WIR>
A;Note: this propeptide fragment remained non-covalently bound to a defective, unclea
R;Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.
```

EMBO J. 8, 1705-1710, 1989
A;Title: A base substitution in the exon of a collagen gene causes alternative splicing
A;Reference number: S09400; MUID:89356643; PMID:2767050
A;Accession: S09400
A;Molecule type: mRNA
A;Residues: 156-183 <WEI>
R;Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A;Title: Isolation and characterization of the cyanogen bromide peptides from the alphal
A;Reference number: A90567; MUID:71038625; PMID:5529814
A;Contents: CNBr0-1, CNBr2, CNBr4, CNBr5
A;Accession: B90567
A;Molecule type: protein
A;Residues: 162-198,'Z',200-201,'Z',203-206,'Z',208-209,'Z',211-228,'B',230,'BB',233,'Z'
A;Experimental source: skin
A;Note: evidence for 170-allysine
R;Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P
Eur. J. Biochem. 192, 153-159, 1990
A;Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle
A;Reference number: S11372; MUID:90382436; PMID:2169412
A;Accession: S11372
A;Molecule type: protein
A;Residues: 175-187;274-287,'P',289 <BAE>
A;Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R;Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
J. Biol. Chem. 266, 21827-21832, 1991
A;Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
ooperative melting of intact type I collagen.
A;Reference number: I55342; MUID:92042092; PMID:1718984
A;Accession: I55342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 258-268;1347-1357 <DEA>
A;Cross-references: GB:S67495; NID:g239007; PIDN:AAB20350.1; PID:g239008
A;Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A;Reference number: A92069; MUID:71001508; PMID:4319110
A;Accession: A92069
A;Molecule type: protein
A;Residues: 263-268 <MOR>
A;Experimental source: skin
A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
R;Labhard, M.E.; Hollister, D.W.
Matrix 10, 124-130, 1990
A;Title: Segmental amplification of the entire helical and telopeptide regions of the cI
A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Accession: S15989
A;Molecule type: mRNA
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
R;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N
Connect. Tissue Res. 29, 1-11, 1993
A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A;Reference number: I52905; MUID:93339042; PMID:8339541
A;Accession: I52905
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 342-352,'C',354-359 <WI2>
A;Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
A;Note: mutant sequence from patient with osteogenesis imperfecta
R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-5223, 1983
A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A;Reference number: A90476; MUID:84080385; PMID:6689127
A;Accession: A90476
A;Molecule type: mRNA
A;Residues: 425-1250,'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>
A;Cross-references: GB:K01228; NID:g180391; PIDN:AAA51995.1; PID:g180392
A;Note: sequence partially completed for missing nucleotides by A29439
R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A;Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type II

A;Reference number: A22161; MUID:85104934; PMID:2981843
A;Accession: A22161
A;Molecule type: DNA
A;Residues: 472-594,'R',596-607 <CH3>
A;Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1;
A;Note: the authors translated the codon CGT for residue 595 as Pro
R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explai

A;Reference number: A35336; MUID:90252792; PMID:2339700
A;Accession: A35336
A;Molecule type: mRNA
A;Residues: 710-720,'E',722-737,'E',739-745 <WAL>
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mot
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in th
A;Reference number: I54365; MUID:95187161; PMID:7881420
A;Accession: I54365
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 746-766,'S',768-781 <FOR>
A;Cross-references: GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID:g1009094
R;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of
A;Reference number: A47426; MUID:93352646; PMID:8349697
A;Accession: A47426
A;Molecule type: mRNA
A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different
A;Accession: B47426
A;Molecule type: mRNA
A;Residues: 1179-1464 <CH4>
A;Experimental source: normal dermal fibroblast culture
A;Accession: C47426
A;Molecule type: mRNA
A;Residues: 1179-1276,'H',1278-1464 <CH5>
A;Experimental source: fetal cell 86-237
A;Accession: D47426
A;Molecule type: mRNA
A;Residues: 1179-1336,1339-1464 <CH6>
A;Experimental source: fetal cell 86-146
A;Accession: E47426
A;Molecule type: mRNA
A;Residues: 1179-1387,'R',1389-1464 <CH7>
A;Experimental source: fetal cell 88-251
R;Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.;
J. Biol. Chem. 263, 14605-14607, 1988
A;Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptid
A;Reference number: I55269; MUID:89008319; PMID:3170557
A;Accession: I55269
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1187-1194,'C',1196-1220 <COH>
A;Cross-references: GB:M23213; NID:g340842; PIDN:AAB59363.1; PID:g499622
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta
R;Maekelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A;Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.

Query Match 9.1%; Score 118.5; DB 1; Length 1464;
Best Local Similarity 36.3%; Pred. No. 0.028;
Matches 33; Conservative 2; Mismatches 23; Indels 33; Gaps 4;

```
Qy          3 PQGPAAS--PQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||  |  || :||         | |      | |                    |||
Db        357 PQGPRGSEGPQGVRG--------EPGPPG----PAG------------------AAGPA 385

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
```

```
              | || || |||    | ||| |  || | :|
Db        386 GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416


RESULT 5
T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29031
R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: Z20555
A;Accession: T29031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-327 <WUX>
A;Cross-references: EMBL:AF003139; PIDN:AAB54156.1; GSPDB:GN00019; CESP:F53G12.7
A;Experimental source: strain Bristol N2; clone F53G12
C;Genetics:
A;Gene: CESP:F53G12.7
A;Map position: 1
A;Introns: 59/3; 138/1; 223/2
C;Superfamily: unassigned collagens

  Query Match             9.0%;  Score 117;  DB 2;  Length 327;
  Best Local Similarity   33.3%;  Pred. No. 0.0069;
  Matches   31;  Conservative    2;  Mismatches   22;  Indels   38;  Gaps    3;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              | ||||                  | |      |:||  |                 |
Db        261 MGPQGP------------------PGPPG----PRGKDGA---------------GGEK 282

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGEC 93
              | ||  |:||    || || || ||  |||| |
Db        283 GAPGDQGNPGPYGKPGQPGAPGPDGSAGEKGGC 315


RESULT 6
A55267
collagen alpha 5(IV) chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999
C;Accession: A55267
R;Zheng, K.; Thorner, P.S.; Marrano, P.; Baumal, R.; McInnes, R.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 3989-3993, 1994
A;Title: Canine X chromosome-linked hereditary nephritis: a genetic model for human X-li
en type IV.
A;Reference number: A55267; MUID:94224868; PMID:8171024
A;Accession: A55267
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-754 <ZHE>
A;Cross-references: GB:U07888; NID:g469547; PIDN:AAB60258.1; PID:g469548
C;Superfamily: collagen alpha 1(IV) chain

  Query Match             9.0%;  Score 117;  DB 2;  Length 754;
  Best Local Similarity   34.4%;  Pred. No. 0.018;
  Matches   33;  Conservative    7;  Mismatches   34;  Indels   22;  Gaps    4;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIP-----KGKQ--KAQLRQREVVDLYNGMC 55
              ||||   |            .|| |     :|     ||::    |  |  :  |
Db        332 PQGPPGRP-----------GLPGPEGPRGLPGNGGIKGERGNPGQPGQPGLPGLKGD-- 377

Qy         56 LQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
               ||| |: |  | || | : | ||:||  || | ||
Db        378 -QGPPGIQGNPGRPGLNGMKGDPGLPGVPGFPGMKG 412


RESULT 7
S28791
collagen alpha 1(XI) chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S28791
R;Nah, H.D.; Barembaum, M.; Upholt, W.B.
J. Biol. Chem. 267, 22581-22586, 1992
A;Title: The chicken alpha1(XI) collagen gene is widely expressed in embryonic tissue
A;Reference number: S28791; MUID:93054557; PMID:1429607
A;Accession: S28791
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-888 <NAH>
A;Cross-references: EMBL:M88593; NID:g211619; PIDN:AAA48707.1; PID:g211620
C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homolo
F;665-887/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

  Query Match             8.9%;  Score 116;  DB 2;  Length 888;
  Best Local Similarity   34.1%;  Pred. No. 0.027;
  Matches   31;  Conservative    4;  Mismatches   20;  Indels   36;  Gaps    3;

Qy          3 PQGPAA--SPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||||    |: |||:          |    |                        ||
Db        479 PQGPAGKPGPEGLRGI----------PGPVGE-----------------------QGLP 504

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
              | ||:|| ||    || ||: |  | |||||
Db        505 GAPGQDGPPGHLGPPGLPGLKGDPGSKGEKG 535


RESULT 8
CGHU3B
collagen alpha 3(IV) chain precursor, long splice form - human
N;Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice for
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: A54763; A43928; A44043; A45971; A39786
R;Mariyama, M.; Leinonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
J. Biol. Chem. 269, 23013-23017, 1994
A;Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpress
A;Reference number: A54763; MUID:94364994; PMID:8083201
A;Accession: A54763
A;Molecule type: mRNA
A;Residues: 1-1670 <MAR>
A;Cross-references: GB:X80031; NID:g577563; PID:g577564
A;Experimental source: kidney
R;Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D.
J. Clin. Invest. 89, 592-601, 1992
A;Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the
A;Reference number: A43928; MUID:92147878; PMID:1737849
A;Accession: A43928
A;Molecule type: mRNA
A;Residues: 1331-1524,'I',1526-1670 <TUR>
A;Cross-references: GB:M81379
A;Experimental source: kidney
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 267, 19780-19784, 1992
A;Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpas
ction.
A;Reference number: A44043; MUID:93015826; PMID:1400291
A;Accession: A44043
A;Molecule type: DNA; mRNA
A;Residues: 1386-1670 <QUI>
A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A;Reference number: A44738; MUID:94274734; PMID:8006044
A;Contents: annotation; erratum; correction to intronic sequence in A44043
R;Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A;Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.
A;Reference number: A45971; MUID:93280184; PMID:8505332
A;Accession: A45971
A;Status: nucleic acid sequence not shown
```

```
A;Molecule type: mRNA
A;Residues: 1427-1444 <BER>
A;Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident
R;Morrison, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T.
Am. J. Hum. Genet. 49, 545-554, 1991
A;Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of
A;Reference number: A39786; MUID:91353570; PMID:1882840
A;Accession: A39786
A;Molecule type: mRNA
A;Residues: 1453-1593,'A',1595-1670 <MOR>
A;Cross-references: GB:S55790; NID:g234418; PIDN:AAB19637.1; PID:g234419
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (
ed and subsequently O-glycosylated.
C;Comment: In Goodpasture's syndrome, an autoimmune response develops against an epitope
C;Genetics:
A;Gene: GDB:COL4A3
A;Cross-references: GDB:128351; OMIM:120070
A;Map position: 2q36-2q37
A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands with
C;Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 3(
mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a
er associations in the interrupted helical domain (with disulfide and desmosine cross-li
C;Function:
A;Description: minor structural component of extracellular basement membrane in kidney g
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extracel
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>
F;29-42/Domain: amino-terminal nonhelical, NH1 <NH1>
F;43-1438/Region: interrupted helical
F;791-793/Region: cell attachment (R-G-D) motif
F;996-998/Region: cell attachment (R-G-D) motif
F;1154-1156/Region: cell attachment (R-G-D) motif
F;1306-1308/Region: cell attachment (R-G-D) motif
F;1345-1347/Region: cell attachment (R-G-D) motif
F;1432-1434/Region: cell attachment (R-G-D) motif
F;1439-1670/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;31,33,39,41,125,422,476,479,682,722,809,1387/Disulfide bonds: interchain #status predi
F;253/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1460-1548,1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F;1505-1511,1616-1622/Disulfide bonds: #status predicted
F;1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted

  Query Match             8.9%;  Score 116;  DB 1;  Length 1670;
  Best Local Similarity   35.1%;  Pred. No. 0.055;
  Matches   33;  Conservative    6;  Mismatches   37;  Indels   18;  Gaps    3;

Qy          5 GPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
              ||   |    |||      :| |     :|       :  |           || ||: |
Db        467 GPKGEP----GLLCTQCPYIPGPPGLPGLPGLHGVKGIPGR----------QGAAGLKG 511

Qy         65 RDGSPGANVIPGTPGIPGRD---GFKGEKGECLR 95
                ||||   :|| || ||     | |||||| |:
Db        512 SPGSPGNTGLPGFPGFPGAQGDPGLKGEKGETLQ 545


RESULT 9
CGHU4B
collagen alpha 1(IV) chain precursor - human
N;Alternate names: procollagen alpha 1(IV) chain
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence_revision 31-Dec-1992 #text_change 07-Dec-1999
C;Accession: S16876; A32117; S02738; S00048; S25826; A23115; S00207; S39614; A02863; A58
R;Soininen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K.
J. Biol. Chem. 264, 13565-13571, 1989
A;Title: Structural organization of the gene for the alpha-1 chain of human type IV coll
A;Reference number: S16876; MUID:89340433; PMID:2701944
A;Accession: S16876
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1669 <SOI1>
A;Cross-references: EMBL:J04217; GB:J05039; NID:g180800; PIDN:AAA53098.1; PID:g180803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1988
R;Soininen, R.; Huotari, M.; Hostikka, S.L.; Prockop, D.J.; Tryggvason, K.
J. Biol. Chem. 263, 17217-17220, 1988
A;Title: The structural genes for alpha1 and alpha2 chains of human type IV collagen
A;Reference number: A92690; MUID:89034231; PMID:3182844
A;Accession: A32117
A;Molecule type: DNA
A;Residues: 1-28 <SOI2>
A;Cross-references: EMBL:J04217; NID:g180759; PIDN:AAA53097.1; PID:g553233
R;Poeschl, E.; Pollner, R.; Kuehn, K.
EMBO J. 7, 2687-2695, 1988
A;Title: The genes for the alpha1(IV) and alpha2(IV) chains of human basement membran
A;Reference number: S02738; MUID:89030632; PMID:2846280
A;Accession: S02738
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6,'L',8-28 <POE>
A;Cross-references: EMBL:X12784; NID:g30072
R;Brazel, D.; Oberbaeumer, I.; Dieringer, H.; Babel, W.; Glanville, R.W.; Deutzmann,
Eur. J. Biochem. 168, 529-536, 1987
A;Title: Completion of the amino acid sequence of the alpha1 chain of human basement
A;Reference number: S00048; MUID:88029471; PMID:3311751
A;Accession: S00048
A;Molecule type: mRNA
A;Residues: 1-318,'A',320-944 <BRA1>
A;Cross-references: EMBL:X05561; NID:g30066; PIDN:CAA29075.1; PID:g30067
A;Accession: S25826
A;Molecule type: protein
A;Residues: 271-318,'A',320-554 <BRA2>
R;Glanville, R.W.; Qian, R.Q.; Siebold, B.; Risteli, J.; Kuehn, K.
Eur. J. Biochem. 152, 213-219, 1985
A;Title: Amino acid sequence of the N-terminal aggregation and cross-linking region (
A;Reference number: A23115; MUID:86004708; PMID:4043082
A;Accession: A23115
A;Molecule type: protein
A;Residues: 28-236,'KE',239-240,'K',242-243 <GLA>
A;Experimental source: placenta
A;Note: the amino end of the mature form is blocked
R;Soininen, R.; Haka-Risku, T.; Prockop, D.J.; Tryggvason, K.
FEBS Lett. 225, 188-194, 1987
A;Title: Complete primary structure of the alpha(1)-chain of human basement membrane
A;Reference number: S00207; MUID:88083584; PMID:3691802
A;Accession: S00207
A;Molecule type: mRNA
A;Residues: 244-530 <SOI3>
A;Cross-references: EMBL:Y00706; NID:g29548; PIDN:CAA68698.1; PID:g29549
R;Eble, J.A.; Golbik, R.; Mann, K.; Kuehn, K.
EMBO J. 12, 4795-4802, 1993
A;Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collag
A;Reference number: S39614; MUID:94038963; PMID:8223488
A;Accession: S39614
A;Molecule type: protein
A;Residues: 371-554 <EBL>
R;Babel, W.; Glanville, R.W.
Eur. J. Biochem. 143, 545-556, 1984
A;Title: Structure of human-basement-membrane (type IV) collagen. Complete amino-acid
A;Reference number: A02863; MUID:85003629; PMID:6434307
A;Accession: A02863
A;Molecule type: protein
A;Residues: 534-718,'D',720-836,'Y',838-841,'P',843-903,'Q',905-913,'K',915-997,'K',9
A;Experimental source: placenta
R;Glanville, R.W.; Rauter, A.
Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A;Title: Pepsin fragments of human placental basement-membrane collagens showing inte
A;Reference number: S16908; MUID:82005835; PMID:6792033
A;Accession: A58517
A;Molecule type: protein
A;Residues: 534-537,'G',539,'G',541-542,'X',544-553;1389-1405,'XX',1408-1409,'X',1411
R;MacWright, R.S.; Benson, V.A.; Lovello, K.T.; van der Rest, M.; Fietzek, P.P.
Biochemistry 22, 4940-4948, 1983
A;Title: Isolation and characterization of pepsin-solubilized human basement membrane
```

A;Reference number: S16910; MUID:84053346; PMID:6416291
A;Accession: S16910
A;Molecule type: protein
A;Residues: 534-537,'G',539,'G',541-542,'G',544-549;939-940,'M',942-944,'V',946,'X',948-
A;Experimental source: placenta
R;Pihlajaniemi, T.; Tryggvason, K.; Myers, J.C.; Kurkinen, M.; Lebo, R.; Cheung, M.C.; P
J. Biol. Chem. 260, 7681-7687, 1985
A;Title: cDNA clones coding for the Pro-alpha-1(IV) chain of human type IV procollagen r
A;Reference number: S01466; MUID:85207819; PMID:2581969
A;Accession: S01466
A;Molecule type: mRNA
A;Residues: 1256-1669 <PIH>
A;Cross-references: EMBL:M10940; NID:g180421; PIDN:AAA52006.1; PID:g180424
R;Brinker, J.M.; Gudas, L.J.; Loidl, H.R.; Wang, S.Y.; Rosenbloom, J.; Kefalides, N.A.;
Proc. Natl. Acad. Sci. U.S.A. 82, 3649-3653, 1985
A;Title: Restricted homology between human alpha-1 type IV and other procollagen chains.
A;Reference number: S16879; MUID:85216555; PMID:2582422
A;Accession: S16879
A;Molecule type: mRNA
A;Residues: 1259-1669 <BRI>
A;Cross-references: EMBL:M11315; NID:g180817; PIDN:AAA52042.1; PID:g180818
R;Oberbaeumer, I.; Laurent, M.; Schwarz, U.; Sakurai, Y.; Yamada, Y.; Vogeli, G.; Voss,
Eur. J. Biochem. 147, 217-224, 1985
A;Title: Amino acid sequence of the non-collagenous globular domain (NC1) of the alpha-1
A;Reference number: A02864; MUID:85127033; PMID:2578961
A;Accession: S19091
A;Molecule type: protein
A;Residues: 1435-1461,'H',1463-1482,'X',1484-1491;1501-1514,'X',1516-1519;1534-1553,'X',
R;Siebold, B.; Deutzmann, R.; Kuehn, K.
Eur. J. Biochem. 176, 617-624, 1988
A;Title: The arrangement of intra- and intermolecular disulfide bonds in the carboxyterm
A;Reference number: S02550; MUID:89005112; PMID:2844531
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:COL4A1
A;Cross-references: GDB:119791; OMIM:120130
A;Map position: 13q34-13q34
A;Introns: 28/3; 48/3; 78/3; 93/3; 108/3; 129/3; 147/3; 156/3; 184/3; 205/3; 217/3; 231/
/1; 731/3; 782/1; 820/1; 876/1; 906/1; 957/1; 990/1; 1020/1; 1066/3; 1109/1; 1136/1; 116
C;Complex: type IV collagen is a heterotrimer of two alpha 1(IV) chains and one alpha 2(
ociations among trimer amino-terminal domains (disulfide and desmosine cross-links), dim
r-trimer associations in the interrupted helical domain (with disulfide and desmosine cr
C;Function:
A;Description: structural component of extracellular basement membrane
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: basement membrane; blocked amino end; cell binding; coiled coil; duplication
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1669/Product: collagen alpha 1(IV) chain #status predicted <MAT>
F;29-162/Domain: amino-terminal nonhelical, 7S <7SD>
F;163-1440/Domain: interrupted helical <COL>
F;414-452/Region: integrin binding #status experimental
F;597-599/Region: cell attachment (R-G-D) motif
F;917-919/Region: cell attachment (R-G-D) motif
F;968-970/Region: cell attachment (R-G-D) motif
F;1441-1669/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;27/Modified site: blocked amino end (Ala) (in mature form) #status experimental
F;31,36,39,41,125,434,467,470/Disulfide bonds: interchain #status predicted
F;45,48,78,90,129,156,172,217,228,231,277,295,298,322,343,361,460,463,497,527,540,543,57
1081,1084,1099,1117,1132,1150,1165,1182,1185,1188,1206,1235,1265,1283,1304,1319,1328,134
F;45,48,78,90,129,156,217,228,231,277,295,298,322,343,361,460,463,497,527,543,573,582,61
99,1117,1132,1150,1165,1182,1185,1188,1206,1235,1265,1283,1304,1319,1328,1340,1356,1371,
F;54,63,75,84,87,96,102,105,108,111,117,120,123,138,141,147,150,153,159,167,178,181,184,
,419,422,425,439,445,448,451,479,485,491,494,503,512,518,524,530,546,549,552,555,561,567
9,745,748,751,754,763/Modified site: 4-hydroxyproline (Pro) #status experimental
F;126/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;129/Modified site: allysine (Lys) #status predicted
F;172,540,947/Modified site: 5-hydroxylysine (Lys) #status atypical
F;272,645,839/Modified site: 4-hydroxyproline (Pro) #status atypical
F;446-447/Cleavage site: Gly-Ile (gelatinase B) #status predicted
F;766,775,784,787,790,796,799,804,810,816,822,834,860,863,869,872,875,887,890,893,899,90
23,1129,1138,1141,1159,1171,1176,1179,1194,1200,1203,1215,1224,1227,1244,1247,1250,1256,
431,1437/Modified site: 4-hydroxyproline (Pro) #status experimental
F;1120,1268/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;1120,1268/Binding site: carbohydrate (Lys) (covalent) (partial) #status experimenta
F;1214,1424/Modified site: 3-hydroxyproline (Pro) #status absent
F;1392,1395,1398,1404/Modified site: 4-hydroxyproline (Pro) #status experimental
F;1460-1548,1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F;1505-1511,1616-1622/Disulfide bonds: #status predicted
F;1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted

Query Match 8.9%; Score 115.5; DB 1; Length 1669;
Best Local Similarity 34.8%; Pred. No. 0.061;
Matches 32; Conservative 5; Mismatches 20; Indels 35; Gaps 4;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLP-APSSASEIPKGKQKAQLRQREVVDLYNGMCLQGP 59
              | | ||   |             || :|  |:| |||                    :||
Db       1212 MGPPGPQGQP-----------GLPGSPGHATEGPKGD-----------------RGP 1240

Qy         60 AGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
                | ||  | ||     | ||:|| || ||:||
Db       1241 QGQPGLPGLPGP---MGPPGLPGIDGVKGDKG 1269
```

RESULT 10
CGHU7L
collagen alpha 1(III) chain precursor - human
N;Alternate names: procollagen alpha 1(III) chain
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511;
R;Prockop, D.J.
submitted to the EMBL Data Library, February 1989
A;Reference number: S05272
A;Accession: S05272
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1240,'V',1242-1466 <PRC>
A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A;Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of h
erences.
A;Reference number: S04642; MUID:89350838; PMID:2764886
A;Accession: S04642
A;Molecule type: mRNA
A;Residues: 1-1196 <ALA>
A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
A;Note: the complete sequence is not shown
R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gen
A;Reference number: PE0011; MUID:89378752; PMID:2777083
A;Accession: PE0011
A;Molecule type: DNA
A;Residues: 1-176 <BEN>
A;Cross-references: GB:M26939; NID:g180813; PIDN:AAA52040.1; PID:g180814
R;Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human
A;Reference number: S01726; MUID:88303360; PMID:3405773
A;Accession: S01726
A;Molecule type: mRNA
A;Residues: 1-170 <TOM>
A;Cross-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061
A;Note: the authors translated the codon CAG for residue 154 as His
R;Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collag
A;Reference number: S04887; MUID:89386015; PMID:2780304
A;Accession: S04887
A;Molecule type: mRNA
A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-6
A;Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleot

R;Seyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977
A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A;Reference number: A90399; MUID:77134724; PMID:557335
A;Accession: A90399
A;Molecule type: protein
A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
submitted to the Atlas, December 1977
A;Reference number: A94562
A;Accession: A94562
A;Molecule type: protein
A;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A;Experimental source: liver
A;Note: author submitted corrections to A90399
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
fspring.
A;Reference number: I51868; MUID:93304430; PMID:8317500
A;Accession: I51868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 186-194 <MIL>
A;Cross-references: GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637
R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A;Reference number: S59511; MUID:96067614; PMID:7487954
A;Accession: S59511
A;Molecule type: mRNA
A;Residues: 302-423 <CHI>
A;Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
R;Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe
A;Reference number: A90414; MUID:79000343; PMID:687591
A;Accession: A90414
A;Molecule type: protein
A;Residues: 399-675,'N',677-727 <SEY3>
A;Experimental source: liver
R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5 of a splice donor site causes skipping of th
A;Reference number: I55349; MUID:91161621; PMID:1672129
A;Accession: I55349
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 537-605 <LEE>
A;Cross-references: GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:g180816
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty
A;Reference number: A90438; MUID:80198282; PMID:6246925
A;Accession: A90438
A;Molecule type: protein
A;Residues: 728-895,'A',897-964 <SEY4>
A;Experimental source: liver
R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan
J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping ar
A;Reference number: A38303; MUID:91009133; PMID:2145268
A;Accession: A38303
A;Molecule type: mRNA
A;Residues: 861-1015 <COL>
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:g
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn
R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A;Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
A;Accession: S02119
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R;Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from
A;Reference number: A90446; MUID:81208139; PMID:7016180
A;Accession: A90446
A;Molecule type: protein
A;Residues: 965-979,'A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',11
A;Experimental source: liver
R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.;
Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procoll
A;Reference number: A93551; MUID:85087944; PMID:6096827
A;Accession: A93551
A;Molecule type: mRNA
A;Residues: 1065-1155,'P',1157-1466 <LOI>
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Br
Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately modulated with the t
A;Reference number: I52393; MUID:86187804; PMID:3754462
A;Accession: I52393
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long
A;Reference number: I59025; MUID:85216505; PMID:3858826
A;Accession: I79359
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1165-1196 <EMA>
A;Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418
R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen
A;Reference number: A92516; MUID:85157600; PMID:2579949
A;Accession: A92516
A;Molecule type: DNA
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons give
ation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequentl
C;Genetics:
A;Gene: GDB:COL3A1
A;Cross-references: GDB:118729; OMIM:120180
A;Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 141
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-
C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfid
er of their length, is formed with desmosine cross-links made from lysine and allysin
C;Function:
A;Description: structural component of extracellular fibrous polymer that maintains i
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-153/Domain: amino-terminal propeptide #status predicted <PRO>
F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
F;154-167/Region: amino-terminal nonhelical telopeptide
F;168-1196/Region: helical
F;1091-1093/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>

```
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;161,1212/Modified site: allysine (Lys) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;948-949/Cleavage site: Gly-Ile (collagenase) #status experimental
F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted

  Query Match             8.8%;  Score 115;  DB 1;  Length 1466;
  Best Local Similarity   36.1%;  Pred. No. 0.058;
  Matches   39;  Conservative    8;  Mismatches   47;  Indels   14;  Gaps    5;

Qy         22 LQLPAPSSASEIPKGKQKAQLRQREVVDLY--NGMCLQGPAGVPGRDGSPGANVIPGTPG 79
              |  | |    ||| |:  |   |      .    ||   ||| | ||  | || |  || ||
Db         72 LDCPNP----EIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPG 127

Qy         80 IPGRDGFKGEKGECLRESF---EESWTPNYKQCSWSSLNYGIDLGKIA 124
                ||  |  |  | |  ||     ::::| |      |   |: :| :|
Db        128 QPGSPGSPGPPGIC--ESCPTGPQNYSPQYDSYDVKS---GVAVGGLA 170


RESULT 11
S16366
collagen alpha 2(IV) chain precursor - pig roundworm
C;Species: Ascaris suum (pig roundworm)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
C;Accession: S16366
R;Pettitt, J.; Kingston, I.B.
J. Biol. Chem. 266, 16149-16156, 1991
A;Title: The complete primary structure of a nematode alpha-2(IV) collagen and the parti
A;Reference number: S16366; MUID:91340768; PMID:1714907
A;Accession: S16366
A;Molecule type: mRNA
A;Residues: 1-1763 <JBI>
A;Cross-references: GB:M67507; NID:g159648; PIDN:AAA18014.1; PID:g159649
C;Genetics:
A;Introns: 229/3; 266/3; 305/3; 360/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1;
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: alternative splicing; basement membrane; cell binding; coiled coil; disulfi
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F;27-42/Domain: non-collagenous NH1 #status predicted <NH1>
F;43-1529/Domain: collagenous #status predicted <COL>
F;197-199/Region: cell attachment (R-G-D) motif
F;1530-1763/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NC1>
F;1530-1638/Domain: repeat NC1 #status predicted <NC11>
F;1639-1763/Domain: repeat NC1 #status predicted <NC12>
F;31,34,39,41,536,539/Disulfide bonds: interchain #status predicted
F;126/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1593-1599,1702-1709/Disulfide bonds: #status predicted

  Query Match             8.8%;  Score 115;  DB 2;  Length 1763;
  Best Local Similarity   25.4%;  Pred. No. 0.072;
  Matches   66;  Conservative   24;  Mismatches   94;  Indels   76;  Gaps   16;

Qy          5 GPAASPQRLRGLLLLLLLQ-LPAPSSASEIPKGKQKAQLRQREVVDLYNGM-CLQGPAGV 62
              ||  :|  :||   |  |  || ||     | |   |: |     | : |   : |  |
Db       1449 GPMGAP-GIRGEKGLPGLDGLPGPSG----PPGFAGAKGR-----DGFPGQPGMPGEKGA 1498

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESF---EESWTPNYKQCS------W-- 111
              ||  | ||   ||| ||:||  |  |  |   :: |   : | |    ||       |
Db       1499 PGLPGFPGIEGIPGPPGLPGPSGPPGPPGPSYKDGFLLVKHSQTSEVPQCPPGMVKLWDG 1558

Qy        112 --------SSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNAC-------CQR 156
                     :  ::  |||    |    :   | :  ||         | |
Db       1559 YSLLYIEGNEKSHNQDLGHAGSC----LSRFSTMPFLF-----CDVNNVCNYASRNDKSY 1609

Qy        157 WYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDV---AI 213
              |  |       : |:|:  :           |   |    |   :||   | :: |    |
Db       1610 WLST------TAPIPMMPV----------SEGGIEPYISRCAVCEA-PANVIAVHSQTI 1651

Qy        214 WVGTCSDYPKGDASTGWNSV 233
                :  | :        ||||:
Db       1652 QIPNCPN--------GWNSL 1663


RESULT 12
T15268
hypothetical protein F59E12.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T15268
R;Johnson, D.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: Z18318
A;Accession: T15268
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-311 <JOH>
A;Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088834; PIDN:AAB54250.1; GSPDB
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.12
A;Map position: 2
A;Introns: 24/2
C;Superfamily: unassigned collagens

  Query Match             8.8%;  Score 114.5;  DB 2;  Length 311;
  Best Local Similarity   51.1%;  Pred. No. 0.011;
  Matches   23;  Conservative    4;  Mismatches   13;  Indels    5;  Gaps    1;

Qy         53 GMC-----LQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGE 92
              | |      ||| | ||  | || : :||||| ||:|| :|  ||
Db        227 GKCDEVNVAQGPPGSPGPPGLPGPDGLPGTPGNPGQDGEQGPAGE 271


RESULT 13
T26185
hypothetical protein W05B2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T26185
R;Gardner, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20166
A;Accession: T26185
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-304 <WIL>
A;Cross-references: EMBL:Z81138; PIDN:CAB03475.1; GSPDB:GN00021; CESP:W05B2.1
A;Experimental source: clone W05B2
C;Genetics:
A;Gene: CESP:W05B2.1
A;Map position: 3
A;Introns: 27/3
C;Superfamily: unassigned collagens

  Query Match             8.8%;  Score 114;  DB 2;  Length 304;
  Best Local Similarity   31.9%;  Pred. No. 0.012;
  Matches   29;  Conservative    5;  Mismatches   25;  Indels   32;  Gaps    2;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV 62
              ||||                  | |: :   | |  :|                 || |
Db        227 PQGP-----------------PGPAGSPGAPGGPGQAG-------------APGPKGP 254

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGEC 93
              |  | |||:  || || ||: |  |||| |
Db        255 SGAPGQPGADGNPGAPGQPGQSGGAGEKGIC 285


RESULT 14
T26184
```

```
hypothetical protein W05B2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T26184
R;Gardner, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20166
A;Accession: T26184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-304 <WIL>
A;Cross-references: EMBL:Z81138; PIDN:CAB03474.1; GSPDB:GN00021; CESP:W05B2.6
A;Experimental source: clone W05B2
C;Genetics:
A;Gene: CESP:W05B2.6
A;Map position: 3
A;Introns: 27/3
C;Superfamily: unassigned collagens

  Query Match             8.8%;  Score 114;  DB 2;  Length 304;
  Best Local Similarity   31.9%;  Pred. No. 0.012;
  Matches   29;  Conservative    5;  Mismatches   25;  Indels   32;  Gaps    2;

Qy          3 PQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV 62
              ||||                  | |: :   | |  :|                  || |
Db        227 PQGP-----------------PGPAGSPGAPGGPGQAG-------------APGPKGP 254

Qy         63 PGRDGSPGANVIPGTPGIPGRDGFKGEKGEC 93
                |  | |||:  || || ||: |  |||| |
Db        255 SGAPGQPGADGNPGAPGQPGQSGGAGEKGIC 285


RESULT 15
S22917
collagen alpha 5(IV) chain precursor, renal splice form - human
N;Alternate names: procollagen alpha 5(IV) chain
N;Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 21-Jul-2000
C;Accession: S22917; A54365; A57079; A37122; I54317; A34850; S18850; I56971; I76598; A35
R;Zhou, J.; Hertz, J.M.; Leinonen, A.; Tryggvason, K.
J. Biol. Chem. 267, 12475-12481, 1992
A;Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and identi
n Alport syndrome patient.
A;Reference number: S22917; MUID:92316923; PMID:1352287
A;Accession: S22917
A;Molecule type: mRNA
A;Residues: 1-967 <ZHO>
A;Cross-references: GB:M90464; NID:g180826; PIDN:AAA52046.1; PID:g553234
R;Zhou, J.; Leinonen, A.; Tryggvason, K.
J. Biol. Chem. 269, 6608-6614, 1994
A;Title: Structure of the human type IV collagen COL4A5 gene.
A;Reference number: A54365; MUID:94165049; PMID:8120014
A;Accession: A54365
A;Molecule type: DNA
A;Residues: 1-922 <ZH2>
A;Cross-references: GB:U04470; NID:g463378; GB:U04520; NID:g463428; PIDN:AAC27816.1; PID
R;Zhou, J.; Mochizuki, T.; Smeets, H.; Antignac, C.; Laurila, P.; de Paepe, A.; Tryggvas
Science 261, 1167-1169, 1993
A;Title: Deletion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited sm
A;Reference number: A57079; MUID:93361972; PMID:8356449
A;Accession: A57079
A;Molecule type: DNA
A;Residues: 1-27 <ZH4>
A;Cross-references: GB:Z37153; NID:g587203; PIDN:CAA85512.1; PID:g587204
R;Pihlajaniemi, T.; Pohjolainen, E.R.; Myers, J.C.
J. Biol. Chem. 265, 13758-13766, 1990
A;Title: Complete primary structure of the triple-helical region and the carboxyl-termin
A;Reference number: A37122; MUID:90337990; PMID:2380186
A;Accession: A37122
A;Molecule type: mRNA
A;Residues: 84-439,'GS',442-624,'LALQ',629-666,'FR',669-887,'R',889-1264,1271-1691 <PIH>
A;Cross-references: GB:J05558; EMBL:M58526; NID:g1314209
A;Note: submitted to the EMBL Data Library, February 1991
A;Note: the authors translated the codon GCC for residue 115 as Val
R;Renieri, A.; Seri, M.; Myers, J.C.; Pihlajaniemi, T.; Massella, L.; Rizzoni, G.; De
Hum. Mol. Genet. 1, 127-129, 1992
A;Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid
A;Reference number: I54317; MUID:93244772; PMID:1363780
A;Accession: I54317
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 313-324,'E',326-330 <REN>
A;Cross-references: GB:S59334; NID:g299946; PIDN:AAD13909.1; PID:g4261609
R;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Tryggvason, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990
A;Title: Identification of a distinct type IV collagen alpha chain with restricted ki
A;Reference number: A34850; MUID:90160375; PMID:1689491
A;Accession: A34850
A;Molecule type: mRNA
A;Residues: 914-1264,1271-1691 <HOS>
A;Cross-references: EMBL:M31115; NID:g180824; PIDN:AAA52045.1; PID:g180825
R;Zhou, J.; Hostikka, S.L.; Chow, L.T.; Tryggvason, K.
Genomics 9, 1-9, 1991
A;Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene t
A;Reference number: A37969; MUID:91169491; PMID:2004755
A;Accession: S18850
A;Molecule type: DNA
A;Residues: 924-1264,1271-1691 <ZH3>
A;Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459;
8; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AAA51558.1;
R;Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Berghe, H.; Cassiman, J.J.
Kidney Int. 44, 1316-1321, 1993
A;Title: Differential splicing of COL4A5 mRNA in kidney and white blood cells: a comp
A;Reference number: I56971; MUID:94133540; PMID:8301933
A;Accession: I56971
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1258-1276 <GUO1>
A;Cross-references: GB:S69168; NID:g545095; PIDN:AAC60612.1; PID:g545096
A;Note: kidney splice form
A;Accession: I76598
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1284-1291,'TFLGYLACLV' <GUO2>
A;Cross-references: GB:S69169; NID:g545097; PIDN:AAC60613.1; PID:g545098
A;Note: frameshift mutation in patient with Alport syndrome
R;Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, A.S.; Goddard, A.D.; Sheer, D.;
Am. J. Hum. Genet. 46, 1024-1033, 1990
A;Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the r
A;Reference number: A35335; MUID:90252791; PMID:2339699
A;Accession: A35335
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1448-1477 <MYE>
R;Nakazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Koitabashi, Y.; Takada, T.;
Kidney Int. 46, 1307-1314, 1994
A;Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in prim
A;Reference number: I56975; MUID:95156893; PMID:7853788
A;Accession: I56975
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1595-1602 <NAK>
A;Cross-references: GB:S75903; NID:g913882; PIDN:AAB33374.1; PID:g913883
A;Note: permature termination mutation from a patient with Alport syndrome; one other
R;Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Tryggvason, K
Genomics 17, 485-489, 1993
A;Title: Identification of four novel mutations in the COL4A5 gene of patients with A
A;Reference number: I54188; MUID:94010948; PMID:8406498
A;Accession: I54188
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1604-1607,'VHDAYKC' <LEM>
A;Cross-references: GB:S65767; NID:g425563; PIDN:AAD13967.1; PID:g4261667
A;Note: frameshift mutation from a patient with Alport syndrome; five other mutations
C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
```

ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: GDB:COL4A5; ATS
A;Cross-references: GDB:120596; OMIM:303630
A;Map position: Xq22-Xq22
A;Introns: 27/3; 47/3; 77/3; 92/3; 107/3; 128/3; 146/3; 155/3; 182/3; 203/3; 215/3; 229/
/3; 799/1; 837/1; 893/1; 923/1; 973/1; 1006/1; 1036/1; 1082/3; 1125/1; 1152/1; 1185/1; 1
A;Note: the alpha 5(IV) and alpha 6(IV) chain genes are encoded on opposite strands with
C;Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 5(
mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a
er associations in the interrupted helical domain (with disulfide and desmosine cross-li
C;Function:
A;Description: minor structural component of extracellular basement membrane
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: Alport syndrome; basement membrane; coiled coil; extracellular matrix; glyco
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1691/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <MAT1
F;27-1264,1271-1691/Product: collagen alpha 5(IV) chain, leukocyte splice form #status p
F;27-41/Domain: amino-terminal nonhelical, NC2 #status predicted <NC2>
F;42-1462/Region: interrupted helical
F;1463-1691/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <NC1>
F;1473-1573/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1583-1687/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;29,32,38,40,124,451,481,484/Disulfide bonds: interchain #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1482-1570,1515-1573/Disulfide bonds: (or 1482-1573, 1515-1570) #status predicted
F;1527-1533,1638-1644/Disulfide bonds: #status predicted
F;1592-1684,1626-1687/Disulfide bonds: (or 1592-1687, 1626-1684) #status predicted

Query Match 8.8%; Score 114; DB 1; Length 1691;
Best Local Similarity 35.4%; Pred. No. 0.084;
Matches 34; Conservative 7; Mismatches 39; Indels 16; Gaps 4;

```
Qy          3 PQGPAA--SPQRLRGLLLLLLLQLPAPSSASEIP-----KGKQKAQLRQREVVDLYNGMC 55
              ||||     |   :|        || |     :|     || :|    |  :  |
Db       1256 PQGPPGRPGPTGFQG--------LPGPEGPPGLPGNGGIKG-EKGNPGQPGLPGLPGLKG 1306

Qy         56 LQGPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKG 91
                ||| |: |  | || | : | ||:||  || | ||
Db       1307 DQGPPGLQGNPGRPGLNGMKGDPGLPGVPGFPGMKG 1342
```

Search completed: August 13, 2003, 13:28:06
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:28:12 ; Search time 85 Seconds
(without alignments)
453.771 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 6118

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	243	100.0	243	21	AAY99441	Human PRO1755 (UNQ
2	243	100.0	243	21	AAY99462	Human PRO1550 amin
3	243	100.0	243	22	AAU29206	Human PRO polypept
4	243	100.0	243	22	AAB87586	Human PRO1550. Ho
5	243	100.0	243	22	AAB66190	Protein of the inv
6	243	100.0	243	22	AAB66211	Protein of the inv
7	243	100.0	243	23	ABP68636	Human pancreatic c
8	243	100.0	243	23	ABG95911	Human secreted/tra
9	243	100.0	243	23	ABG78938	Human breast tumou
10	243	100.0	243	23	ABB95545	Human angiogenesis
11	243	100.0	243	23	AAE20462	Human tumour-assoc
12	243	100.0	243	23	ABB84939	Human PRO1550 prot
13	243	100.0	243	24	ABU71294	Human PRO1550 prot
14	243	100.0	243	24	ABU71566	Human secreted pol
15	243	100.0	243	24	ABU72012	Novel human secret
16	243	100.0	243	24	ABU72169	Human PRO polypept
17	243	100.0	243	24	ABU65751	Human secreted/tra
18	243	100.0	243	24	ABU66084	Novel human secret
19	243	100.0	243	24	ABU67588	Human secreted/tra
20	243	100.0	243	24	ABG75948	Human antigenic ta
21	243	100.0	243	24	ABU65446	Human PRO polypept
22	243	100.0	243	24	ABJ37761	Human tumour-relat
23	243	100.0	243	24	ABU58582	Human PRO polypept
24	243	100.0	243	24	ABU56118	Human secreted/tra
25	243	100.0	243	24	ABU57113	Human PRO polypept
26	243	100.0	243	24	ABU10692	Human secreted/tra
27	243	100.0	278	23	ABP68637	Human pancreatic c
28	243	100.0	278	23	ABG78939	Human breast tumou
29	243	100.0	278	24	ABJ37762	Human tumour-relat
30	197	81.1	197	23	ABG78940	Human breast tumou
31	197	81.1	197	24	ABJ37763	Human tumour-relat
32	197	81.1	232	23	ABG78941	Human breast tumou
33	197	81.1	232	24	ABJ37764	Human tumour-relat
34	170	70.0	210	23	ABG96339	Human ovarian canc
35	170	70.0	243	22	AAB36667	Human secretory pr
36	170	70.0	243	23	ABG96340	Human ovarian canc
37	170	70.0	243	23	ABJ05554	Breast cancer-asso
38	170	70.0	243	23	ABB80978	Human REMODELIN po
39	170	70.0	243	24	ABR48227	Human bladder canc
40	170	70.0	243	24	ABG75758	Human REMODELIN pr
41	170	70.0	243	24	ABU56607	Lung cancer-associ
42	170	70.0	276	20	AAW88934	Polypeptide fragme
43	170	70.0	276	22	ABB51005	Human secreted pro
44	170	70.0	278	21	AAB08856	Amino acid sequenc
45	170	70.0	278	22	AAM25746	Human protein sequ

ALIGNMENTS

RESULT 1
AAY99441
ID AAY99441 standard; Protein; 243 AA.
XX
AC AAY99441;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1755 (UNQ828) amino acid sequence SEQ ID NO:352.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.

PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR N-PSDB; AAA37123.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 12; Fig 204; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 243; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
                |||
Db        241 LPK 243


RESULT 2
AAY99462
ID   AAY99462 standard; Protein; 243 AA.
XX
AC   AAY99462;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Human PRO1550 amino acid sequence SEQ ID NO:431.
XX
KW   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW   transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS   Homo sapiens.
XX
PN   WO200012708-A2.
XX
PD   09-MAR-2000.
XX
PF   01-SEP-1999;   99WO-US20111.
XX
PR   01-SEP-1998;   98US-0098716.
PR   01-SEP-1998;   98US-0098749.
PR   01-SEP-1998;   98US-0098750.
PR   02-SEP-1998;   98US-0098803.
PR   02-SEP-1998;   98US-0098821.
PR   02-SEP-1998;   98US-0098843.
PR   09-SEP-1998;   98US-0099536.
PR   09-SEP-1998;   98US-0099596.
PR   09-SEP-1998;   98US-0099598.
PR   09-SEP-1998;   98US-0099602.
PR   09-SEP-1998;   98US-0099642.
PR   10-SEP-1998;   98US-0099741.
PR   10-SEP-1998;   98US-0099754.
PR   10-SEP-1998;   98US-0099763.
PR   10-SEP-1998;   98US-0099792.
PR   10-SEP-1998;   98US-0099808.
PR   10-SEP-1998;   98US-0099812.
PR   10-SEP-1998;   98US-0099815.
PR   10-SEP-1998;   98US-0099816.
PR   15-SEP-1998;   98US-0100385.
PR   15-SEP-1998;   98US-0100388.
PR   15-SEP-1998;   98US-0100390.
PR   16-SEP-1998;   98US-0100584.
PR   16-SEP-1998;   98US-0100627.
PR   16-SEP-1998;   98US-0100661.
PR   16-SEP-1998;   98US-0100662.
PR   16-SEP-1998;   98US-0100664.
PR   17-SEP-1998;   98US-0100683.
PR   17-SEP-1998;   98US-0100684.
PR   17-SEP-1998;   98US-0100710.
PR   17-SEP-1998;   98US-0100711.
PR   17-SEP-1998;   98US-0100919.
PR   17-SEP-1998;   98US-0100930.
PR   18-SEP-1998;   98US-0100848.
PR   18-SEP-1998;   98US-0100849.
PR   18-SEP-1998;   98US-0101014.
PR   18-SEP-1998;   98US-0101068.
PR   18-SEP-1998;   98US-0101071.
PR   22-SEP-1998;   98US-0101279.
PR   23-SEP-1998;   98US-0101471.
PR   23-SEP-1998;   98US-0101472.
PR   23-SEP-1998;   98US-0101474.
PR   23-SEP-1998;   98US-0101475.
PR   23-SEP-1998;   98US-0101476.
PR   23-SEP-1998;   98US-0101477.
PR   23-SEP-1998;   98US-0101479.
PR   24-SEP-1998;   98US-0101738.
PR   24-SEP-1998;   98US-0101741.
PR   24-SEP-1998;   98US-0101743.
PR   24-SEP-1998;   98US-0101915.
PR   24-SEP-1998;   98US-0101916.
PR   29-SEP-1998;   98US-0102207.
PR   29-SEP-1998;   98US-0102240.
PR   29-SEP-1998;   98US-0102307.
PR   29-SEP-1998;   98US-0102330.
PR   29-SEP-1998;   98US-0102331.
PR   30-SEP-1998;   98US-0102484.
PR   30-SEP-1998;   98US-0102487.
PR   30-SEP-1998;   98US-0102570.
PR   30-SEP-1998;   98US-0102571.
PR   01-OCT-1998;   98US-0102684.
PR   01-OCT-1998;   98US-0102687.
PR   02-OCT-1998;   98US-0102965.
PR   06-OCT-1998;   98US-0103258.
PR   06-OCT-1998;   98US-0103449.
PR   07-OCT-1998;   98US-0103314.
PR   07-OCT-1998;   98US-0103315.
PR   07-OCT-1998;   98US-0103328.
PR   07-OCT-1998;   98US-0103395.
PR   07-OCT-1998;   98US-0103396.
PR   07-OCT-1998;   98US-0103401.
PR   08-OCT-1998;   98US-0103633.
PR   08-OCT-1998;   98US-0103678.
PR   08-OCT-1998;   98US-0103679.
PR   08-OCT-1998;   98US-0103711.
PR   14-OCT-1998;   98US-0104257.
PR   20-OCT-1998;   98US-0104987.
PR   20-OCT-1998;   98US-0105000.
PR   20-OCT-1998;   98US-0105002.
PR   21-OCT-1998;   98US-0105104.
PR   22-OCT-1998;   98US-0105169.
PR   22-OCT-1998;   98US-0105266.
PR   26-OCT-1998;   98US-0105693.
PR   26-OCT-1998;   98US-0105694.
PR   27-OCT-1998;   98US-0105807.
PR   27-OCT-1998;   98US-0105881.
PR   27-OCT-1998;   98US-0105882.
PR   27-OCT-1998;   98US-0106062.
PR   28-OCT-1998;   98US-0106023.
PR   28-OCT-1998;   98US-0106029.
PR   28-OCT-1998;   98US-0106030.
PR   28-OCT-1998;   98US-0106032.
PR   28-OCT-1998;   98US-0106033.
PR   28-OCT-1998;   98US-0106178.
PR   29-OCT-1998;   98US-0106248.
PR   29-OCT-1998;   98US-0106384.
PR   29-OCT-1998;   98US-0108500.
PR   30-OCT-1998;   98US-0106464.
PR   03-NOV-1998;   98US-0106856.
PR   03-NOV-1998;   98US-0106902.
PR   03-NOV-1998;   98US-0106905.
PR   03-NOV-1998;   98US-0106919.
PR   03-NOV-1998;   98US-0106932.
PR   03-NOV-1998;   98US-0106934.
PR   10-NOV-1998;   98US-0107783.
PR   17-NOV-1998;   98US-0108775.
PR   17-NOV-1998;   98US-0108779.
PR   17-NOV-1998;   98US-0108787.
PR   17-NOV-1998;   98US-0108788.
```

```
PR   17-NOV-1998;   98US-0108801.
PR   17-NOV-1998;   98US-0108802.
PR   17-NOV-1998;   98US-0108806.
PR   17-NOV-1998;   98US-0108807.
PR   17-NOV-1998;   98US-0108867.
PR   17-NOV-1998;   98US-0108925.
PR   18-NOV-1998;   98US-0108848.
PR   18-NOV-1998;   98US-0108849.
PR   18-NOV-1998;   98US-0108850.
PR   18-NOV-1998;   98US-0108851.
PR   18-NOV-1998;   98US-0108852.
PR   18-NOV-1998;   98US-0108858.
PR   18-NOV-1998;   98US-0108904.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   N-PSDB; AAA37144.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or
PT   secreted PRO polypeptides, useful for screening of potential peptide or
PT   small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS   Claim 12; Fig 246; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC   PCR primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 243;  DB 21;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 3
AAU29206
ID   AAU29206 standard; Protein; 243 AA.
XX
AC   AAU29206;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #183.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46107.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 11; Fig 366; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
```

```
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 243;  DB 22;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 4
AAB87586
ID   AAB87586 standard; Protein; 243 AA.
XX
AC   AAB87586;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1550.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92118.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping.
XX
PS   Claim 12; Fig 122; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 243;  DB 22;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 5
AAB66190
ID   AAB66190 standard; protein; 243 AA.
XX
AC   AAB66190;
XX
DT   02-APR-2001  (first entry)
XX
DE   Protein of the invention #102.
XX
KW   Secreted; transmembrane; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US04342.
XX
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
```

```
PR   01-SEP-1999;   99WO-US20111.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy -
XX
PS   Claim 1; Fig 204; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of
CC   anti-sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents.
CC   The nucleic acids may also be used in gene therapy.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 243;  DB 22;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 6
AAB66211
ID   AAB66211 standard; protein; 243 AA.
XX
AC   AAB66211;
XX
DT   02-APR-2001  (first entry)
XX
DE   Protein of the invention #123.
XX
KW   Secreted; transmembrane; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US04342.
XX
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   01-SEP-1999;   99WO-US20111.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy -
XX
PS   Claim 1; Fig 246; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of
CC   anti-sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents.
CC   The nucleic acids may also be used in gene therapy.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 243;  DB 22;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 7
ABP68636
ID   ABP68636 standard; Protein; 243 AA.
XX
AC   ABP68636;
XX
DT   14-JAN-2003  (first entry)
```

```
XX
DE   Human pancreatic cancer expressed protein SEQ ID NO 4559.
XX
KW   Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW   cytostatic; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200260317-A2.
XX
PD   08-AUG-2002.
XX
PF   30-JAN-2002; 2002WO-US02781.
XX
PR   30-JAN-2001; 2001US-265305P.
PR   31-JAN-2001; 2001US-265682P.
PR   09-FEB-2001; 2001US-267568P.
PR   21-MAR-2001; 2001US-278651P.
PR   28-APR-2001; 2001US-287112P.
PR   16-MAY-2001; 2001US-291631P.
PR   12-JUL-2001; 2001US-305484P.
PR   20-AUG-2001; 2001US-313999P.
PR   27-NOV-2001; 2001US-333626P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Benson DR,  Kalos MD,  Lodes MJ,  Persing DH,  Hepler WT,  Jiang Y;
XX
DR   WPI; 2002-627435/67.
DR   N-PSDB; ABV99144.
XX
PT   New isolated polynucleotide and pancreatic tumor polypeptides, useful
PT   for diagnosing, preventing and/or treating cancer, particularly
PT   pancreatic cancer  -
XX
PS   Claim 2; SEQ ID NO 4559; 300pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising: (a)
CC   any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC   (b) complements of (a); (c) sequences consisting of at least 20
CC   contiguous residues of (a); (d) sequences that hybridize to (a), under
CC   moderately stringent conditions; (e) sequences having at least 75% or 90%
CC   identity to (a); or (f) degenerate variants of (a). Polypeptides
CC   (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
CC   detect cancer in a patient and compositions comprising polypeptides,
CC   polynucleotides, antibodies, fusion proteins, T cell populations and
CC   antigen presenting cells expressing the polypeptide are useful in
CC   treating pancreatic cancer and stimulating an immune response. The
CC   polynucleotides can be used as probes or primers for nucleic acid
CC   hybridisation, in the design and preparation of ribozyme molecules for
CC   inhibiting expression of the tumour polypeptides and proteins in the
CC   tumour cells, in vaccines and for gene therapy.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   243 AA;

  Query Match           100.0%;  Score 243;  DB 23;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 8
ABG95911
ID   ABG95911 standard; Protein; 243 AA.
XX
AC   ABG95911;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human secreted/transmembrane protein PRO1550.
XX
KW   Human; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-0006867.
XX
PR   29-OCT-1997;   97US-063435P.
PR   29-OCT-1997;   97US-064215P.
PR   22-APR-1998;   98US-082797P.
PR   29-APR-1998;   98US-083495P.
PR   15-MAY-1998;   98US-085579P.
PR   10-JUN-1998;   98US-088811P.
PR   10-JUN-1998;   98US-088824P.
PR   10-JUN-1998;   98US-088825P.
PR   11-JUN-1998;   98US-088863P.
PR   12-JUN-1998;   98US-089105P.
PR   16-JUN-1998;   98US-089514P.
PR   16-SEP-1998;   98WO-US19330.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21194.
PR   22-DEC-1999;   99WO-US30720.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   30-MAR-2000; 2000WO-US08439.
PR   22-MAY-2000; 2000WO-US14042.
PR   02-JUN-2000; 2000WO-US15264.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32378.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-731348/79.
DR   N-PSDB; ABS74438.
```

```
XX
PT   New isolated secreted and transmembrane PRO polypeptide useful for
PT   modulating biological activity of a cell, or for treating
PT   sports-related joint problems, osteoarthritis or rheumatoid arthritis
XX
PS   Claim 20; Fig 122; 399pp; English.
XX
CC   The invention relates to an isolated secreted and transmembrane PRO
CC   polypeptide having 80 % sequence identity to a sequence appearing
CC   as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
CC   an extracellular domain of the proteins with their associated signal
CC   peptide or lacking its associated signal peptide. Also included are
CC   the nucleic acids encoding the proteins, vectors, host cells,
CC   fusion proteins and antibodies which specifically bind to the proteins.
CC   The proteins are useful for detecting a polypeptide designated as A, B, C
CC   or D in a sample suspected of containing an A, B, C or D polypeptide,
CC   by contacting the sample with a polypeptide designated as E, F, G, H or
CC   I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
CC   or D/I polypeptide conjugate in the sample, where the formation of the
CC   conjugate is indicative of the presence of an A, B, C or D polypeptide
CC   in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
CC   polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
CC   E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
CC   polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
CC   polypeptide. The sample comprises a cell suspected of expressing the A,
CC   B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
CC   a detectable label or is attached to a solid support. The proteins are
CC   useful for linking a bioactive molecule to a cell expressing a
CC   polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
CC   molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
CC   causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
CC   against them are useful for modulating a biological activity of a cell
CC   expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
CC   I. The cell is killed. The proteins are useful for identifying
CC   agonists or antagonists, for the preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the proteins, as
CC   molecular weight markers for protein electrophoresis purposes, and as
CC   therapeutic agents for treating sports-related joint problems,
CC   articular cartilage defects, osteoarthritis or rheumatoid arthritis.
CC   Nucleic acids encoding the proteins are useful as hybridisation probes,
CC   in chromosome and gene mapping, in the generation of anti-sense RNA and
CC   DNA, for the preparation of the proteins, to generate transgenic or
CC   knockout animals which are useful in the development and screening of
CC   therapeutic useful reagents, for chromosome identification, and in gene
CC   therapy. The antibody is useful as a therapeutic agent, in a diagnostic
CC   assay and for affinity purification of the protein from recombinant
CC   cell culture natural sources. The present sequence represents a novel
CC   secreted or transmembrane protein of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 243;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 9
ABG78938
ID   ABG78938 standard; Protein; 243 AA.
XX
AC   ABG78938;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human breast tumour polypeptide #29.
XX
KW   Human; breast tumour protein; breast cancer; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2002085998-A1.
XX
PD   04-JUL-2002.
XX
PF   13-APR-2001; 2001US-0834759.
XX
PR   28-DEC-1998;   98US-0222575.
PR   02-APR-1999;   99US-0285480.
PR   23-JUN-1999;   99US-0339338.
PR   02-SEP-1999;   99US-0389681.
PR   03-NOV-1999;   99US-0433826.
PR   17-APR-2000; 2000US-0551621.
PR   08-JUN-2000; 2000US-0590751.
PR   22-JUN-2000; 2000US-0604287.
PR   20-JUL-2000; 2000US-0620405.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Jiang Y,  Dillon DC,  Mitcham JL,  Xu J,  Harlocker SL,  Hepler WT;
PI   Henderson RA;
XX
DR   WPI; 2002-635657/68.
DR   N-PSDB; ABS64028, ABS64029.
XX
PT   Novel breast cancer polynucleotides and polypeptides encoded by the
PT   polynucleotides, useful for detecting the presence of breast cancer in
PT   a patient, and in pharmaceutical compositions, for treating breast
PT   cancer -
XX
PS   Claim 2; Page 235-236; 247pp; English.
XX
CC   The invention relates to an isolated breast tumour polynucleotide and the
CC   polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC   detecting the presence of breast cancer in a patient, and in
CC   pharmaceutical compositions for treating breast cancer. The sequences are
CC   useful for stimulating an immune response in a patient and can therefore
CC   be used in production of vaccines. The sequences are also useful for
CC   detecting the presence of a cancer in a patient, by obtaining a
CC   biological sample from the patient, contacting the biological sample with
CC   a composition of the invention and detecting the amount of polynucleotide
CC   that hybridizes to the sample. This sequence represents a human breast
CC   tumour polypeptide of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 243;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
```

```
Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 10
ABB95545
ID ABB95545 standard; Protein; 243 AA.
XX
AC ABB95545;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1550 SEQ ID NO: 246.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95683.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 246; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 243; DB 23; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 11
AAE20462
ID AAE20462 standard; Protein; 243 AA.
XX
AC AAE20462;

```
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human tumour-associated antigenic target-170 (TAT170) protein.
XX
KW   Human; tumour-associated antigenic target-170; TAT170; cytostatic;
KW   gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Signal_peptide
FT   Protein         31..243
FT                   /label= Mature_TAT170_protein
FT   Modified-site   67..72
FT                   /note= "N-myristoylation site"
FT   Modified-site   117..122
FT                   /note= "N-myristoylation site"
FT   Modified-site   163..168
FT                   /note= "N-myristoylation site"
FT   Modified-site   186..189
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   199..204
FT                   /note= "N-myristoylation site"
FT   Modified-site   203..208
FT                   /note= "N-myristoylation site"
XX
PN   WO200216602-A2.
XX
PD   28-FEB-2002.
XX
PF   23-AUG-2001; 2001WO-US26626.
XX
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Goddard A,  Godowski PJ,  Gurney AL,  Polakis P;
PI   Williams PM,  Wood WI,  Wu TD,  Zhang Z;
XX
DR   WPI; 2002-292065/33.
DR   N-PSDB; AAD32717.
XX
PT   New antibodies that bind tumor-associated antigenic target (TAT)
PT   polypeptides, useful for treating and diagnosing tumor (e.g. breast,
PT   lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
PT   pigs, goats, rabbits or humans  -
XX
PS   Claim 1; Fig 7; 124pp; English.
XX
CC   The present invention relates to an isolated antibody that binds to
CC   tumor-associated antigenic target (TAT) polypeptide. The antibody is
CC   used for treating and diagnosing tumours (e.g. breast, lung, liver or
CC   stomach tumours) in mammals, e.g. dogs, cats, cattle, horses, sheep,
CC   pigs, goats, rabbits, or preferably humans. The antibody may also be
CC   used in antibody-dependent enzyme mediated prodrug therapy (ADEPT).
CC   The antibody is also useful for the therapeutic treatment or for the
CC   diagnostic detection of cancer. TAT cDNA is useful in gene therapy.
CC   The present sequence is human TAT170 protein. TAT170 cDNA is designated
CC   as DNA76393-1664.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 243;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 12
ABB84939
ID   ABB84939 standard; Protein; 243 AA.
XX
AC   ABB84939;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO1550 protein sequence SEQ ID NO:246.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US19692.
XX
PR   23-JUN-2000; 2000US-213637P.
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
```

PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88194.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 246; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 243; DB 23; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 13
ABU71294
ID ABU71294 standard; Protein; 243 AA.
XX
AC ABU71294;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO1550 protein.
XX
KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.

PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.
PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 243; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
```

```
Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
ABU71566
ID   ABU71566 standard; Protein; 243 AA.
XX
AC   ABU71566;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Human secreted polypeptide PRO1550.
XX
KW   Human; gene therapy; tumour; cancer.
XX
OS   Homo sapiens.
XX
PN   US2003013855-A1.
XX
PD   16-JAN-2003.
XX
PF   03-MAY-2002; 2002US-0063616.
XX
PR   30-DEC-1998;   98KR-0062142.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   30-DEC-1999;   99WO-US31274.
PR   18-FEB-2000; 2000WO-US04341.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   21-MAR-2000; 2000WO-US07532.
PR   22-MAY-2000; 2000WO-US14042.
PR   02-JUN-2000; 2000WO-US15264.
PR   24-AUG-2000; 2000WO-US23328.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   14-MAY-1999;   99US-0311832.
PR   25-AUG-1999;   99US-0380137.
PR   25-AUG-1999;   99US-0380138.
PR   25-AUG-1999;   99US-0380139.
PR   25-AUG-1999;   99US-0380142.
PR   15-SEP-1999;   99US-0397342.
PR   18-OCT-1999;   99US-0403297.
PR   12-NOV-1999;   99US-0423844.
PR   22-AUG-2000; 2000US-0644848.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   08-NOV-2000; 2000US-0709238.
PR   20-DEC-2000; 2000US-0747259.
PR   22-MAR-2001; 2001US-0816744.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   30-MAY-2001; 2001US-0870574.
PR   05-JUN-2001; 2001US-0874503.
PR   29-JUN-2001; 2001US-0869599.
PR   18-JUL-2001; 2001US-0908827.
PR   06-DEC-2001; 2001US-0006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-330485/31.
DR   N-PSDB; ACA58870.
XX
PT   New isolated antibody specifically binding a PRO polypeptide, useful
PT   for the preparation of a medicament for treating disorders with the
PT   aberrant expression or activity of the PRO polypeptide, such as tumor
PT   conditions and cancer  -
XX
PS   Disclosure; Page 194-195; 406pp; English.
XX
CC   The invention relates to an antibody that binds to a polypeptide with a
CC   fully defined sequence given in the specification. The methods and
CC   compositions (containing antibodies that specifically bind a PRO
CC   polypeptide) of the present invention are useful for the preparation of a
CC   medicament for the treatment of disorders associated with the aberrant
CC   expression or activity of the PRO polypeptide, such as tumour conditions
CC   and cancer. They can also be used to generate transgenic or knockout
CC   animals useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC   molecular weight markers for protein electrophoresis, chromosome
CC   identification and tissue typing. The PRO polypeptides are useful to
CC   induce angiogenesis e.g wound healing; in the treatment of sports-related
CC   joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC   arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC   antibodies may be used in various diagnostic, competitive binding and/or
CC   immunoprecipitation assays. The present sequence represents the amino
CC   acid sequence of a PRO polypeptide of the invention.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 243;  DB 24;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-220;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
ABU72012
ID   ABU72012 standard; Protein; 243 AA.
XX
AC   ABU72012;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1550.
XX
KW   Human; secreted and transmembrane polypeptide;
KW   chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW   therapeutic agent screening; chromosome identification; tissue typing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003018183-A1.
XX
PD   23-JAN-2003.
XX
PF   01-MAY-2002; 2002US-0063512.
```

XX
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR N-PSDB; ACA60423.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody -
XX
PS Disclosure; Fig 122; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO poypeptide.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 243; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 5.1e-220;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

Search completed: August 13, 2003, 13:38:08
Job time : 86 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:35:38 ; Search time 39 Seconds
(without alignments)
599.205 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	3.7	133	2	S57038	probable membrane
2	9	3.7	144	2	T18867	hypothetical prote
3	9	3.7	247	2	A55717	myelin/oligodendro
4	9	3.7	779	1	CGBO1S	collagen alpha 1(I
5	9	3.7	996	2	JE0237	apolipoprotein E r
6	9	3.7	1464	1	CGHU1S	collagen alpha 1(I
7	8	3.3	112	2	A60111	sporozoite antigen
8	8	3.3	141	1	UTHUB	lutropin beta chai
9	8	3.3	165	1	KTHUB	choriogonadotropin
10	8	3.3	169	2	T18321	hypothetical prote
11	8	3.3	177	2	S37749	collagen alpha 2(X
12	8	3.3	249	2	T35724	cobalt transport i
13	8	3.3	254	2	I38427	4-1BB ligand - hum
14	8	3.3	291	2	B60131	homeotic protein X
15	8	3.3	296	2	T24827	hypothetical prote
16	8	3.3	302	2	T21257	hypothetical prote
17	8	3.3	307	2	S36779	ribosome-binding p
18	8	3.3	330	2	S46657	collagen alpha 1(X
19	8	3.3	333	2	T20436	hypothetical prote
20	8	3.3	360	2	T37285	collagen dpy-2 - C
21	8	3.3	365	2	JC7694	soluble-type glyco
22	8	3.3	368	2	AE0086	Fimbrial protein [
23	8	3.3	378	2	T00481	probable RING zinc
24	8	3.3	391	2	D72663	hypothetical prote
25	8	3.3	399	2	C83611	hypothetical prote
26	8	3.3	424	2	C70371	glutamate-1-semial
27	8	3.3	457	1	RWMST4	T-cell surface gly
28	8	3.3	487	1	A26660	steroid 21-monooxy
29	8	3.3	487	2	S54785	cytochrome P450 -
30	8	3.3	500	2	S66522	cartilage matrix p
31	8	3.3	636	2	S41067	collagen alpha 1(I
32	8	3.3	674	2	S23297	collagen alpha 1(X
33	8	3.3	809	2	A46747	Na+/H+-exchanging
34	8	3.3	917	2	S09646	collagen alpha 2(V
35	8	3.3	984	2	S67527	protein kinase (EC
36	8	3.3	1018	1	CGHU2A	collagen alpha 2(V
37	8	3.3	1029	1	S21369	collagen alpha 2(V
38	8	3.3	1102	2	JH0717	guanylate cyclase
39	8	3.3	1108	2	A55915	guanylate cyclase
40	8	3.3	1120	2	H88449	protein F54D8.1 [i
41	8	3.3	1265	1	A37967	neural cell adhesi
42	8	3.3	1278	2	T30188	Niemann-Pick C dis
43	8	3.3	1388	2	A53317	collagen alpha 1(X
44	8	3.3	1414	1	S23809	collagen alpha 2(I
45	8	3.3	1433	2	A46053	bullous pemphigoid

ALIGNMENTS

RESULT 1
S57038
probable membrane protein YJR023c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C;Accession: S57038; S57041; S55212
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56771
A;Accession: S57038
A;Molecule type: DNA
A;Residues: 1-133 <ZAG>
A;Cross-references: EMBL:Z49522; NID:g1015659; PID:g1015661
R;Zagulski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; He
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57040
A;Accession: S57041
A;Molecule type: DNA
A;Residues: 1-93 <HUA>
A;Cross-references: EMBL:Z49522; MIPS:YJR023c
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55183
A;Accession: S55212
A;Molecule type: DNA
A;Residues: 1-133 <DEH>
A;Cross-references: EMBL:X87611
C;Genetics:
A;Cross-references: SGD:S0003784
A;Map position: 10R
C;Superfamily: Saccharomyces probable membrane protein YJR023c
C;Keywords: transmembrane protein

Query Match 3.7%; Score 9; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLLQL 24
|||||||||
Db 22 LLLLLLLQL 30

RESULT 2
T18867
hypothetical protein C02F4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T18867
R;Cummings, P.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19034

A;Accession: T18867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-144 <WIL>
A;Cross-references: EMBL:Z81032; PIDN:CAB02722.1; GSPDB:GN00022; CESP:C02F4.3
A;Experimental source: clone C02F4
C;Genetics:
A;Gene: CESP:C02F4.3
A;Map position: 4
A;Introns: 3/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C02F4.3

Query Match 3.7%; Score 9; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLLQL 24
|||||||||
Db 67 LLLLLLLQL 75

RESULT 3
A55717
myelin/oligodendrocyte glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
C;Accession: A55717; C47712
R;Daubas, P.; Pham-Dinh, D.; Dautigny, A.
Genomics 23, 36-41, 1994
A;Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein ge
A;Reference number: A55717; MUID:95130110; PMID:7829100
A;Accession: A55717
A;Molecule type: DNA
A;Residues: 1-247 <DAU>
A;Cross-references: GB:L29498
R;Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarotti, P.; Roeckel, N.;
Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
A;Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobul
A;Reference number: A47712; MUID:93376728; PMID:8367453
A;Accession: C47712
A;Molecule type: mRNA
A;Residues: 30-95,'E',97-247 <PHA>
A;Cross-references: GB:L20942; NID:g399588; PIDN:AAA03180.1; PID:g399589
C;Genetics:
A;Gene: MOG
A;Map position: 17
A;Note: encoded within the MHC
C;Function:
A;Description: may be involved in lipid interaction; may be involved in cell-cell commun
C;Keywords: glycoprotein; myelin; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>
F;151-179/Domain: transmembrane #status predicted <TM1>
F;204-229/Domain: transmembrane #status predicted <TM2>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.7%; Score 9; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLLQL 24
|||||||||
Db 16 LLLLLLLQL 24

RESULT 4
CGBO1S
collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A91193; A91229; A91387; A91211; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Furthmayr, H.
Eur. J. Biochem. 27, 231-237, 1972
A;Title: Structural characterization of N-terminal antigenic determinants in calf and
A;Reference number: A91193; MUID:72255334; PMID:4115172
A;Accession: A91193
A;Molecule type: protein
A;Residues: 1-19 <RAU>
A;Experimental source: skin
A;Note: the epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is co
R;Fietzek, P.P.; Kuehn, K.
Eur. J. Biochem. 52, 77-82, 1975
A;Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-brom
A;Reference number: A91229; MUID:76022320; PMID:1164916
A;Accession: A91229
A;Molecule type: protein
A;Residues: 20-145 <FIE>
A;Experimental source: skin
A;Note: Lys-103 is hydroxylated and binds glucosylgalactose
R;Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
FEBS Lett. 26, 74-76, 1972
A;Title: The covalent structure of collagen: amino acid sequence of alpha1-CB3 from c
A;Reference number: A91387; MUID:73049499; PMID:4673951
A;Accession: A91387
A;Molecule type: protein
A;Residues: 146-294 <FI2>
A;Experimental source: skin
R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Biochem. 38, 396-400, 1973
A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alpha1-CB7
A;Reference number: A91211; MUID:74086118; PMID:4359390
A;Accession: A91211
A;Molecule type: protein
A;Residues: 295-562 <FI3>
A;Experimental source: skin
R;Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
Eur. J. Biochem. 30, 169-183, 1972
A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 resid
A;Reference number: A91201; MUID:73042276; PMID:4343808
A;Accession: A91201
A;Molecule type: protein
A;Residues: 563-675 <WEN>
A;Experimental source: skin
R;Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
Eur. J. Biochem. 30, 163-168, 1972
A;Title: The covalent structure of collagen. Amino acid sequence of peptide alpha1-CB
A;Reference number: A91200; MUID:73042275; PMID:4343807
A;Accession: A91200
A;Molecule type: protein
A;Residues: 676-758 <FI4>
A;Experimental source: skin
A;Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in pos
R;Rauterberg, J.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K.
FEBS Lett. 21, 75-79, 1972
A;Title: The amino acid sequence of the carboxyterminal nonhelical cross link region
A;Reference number: A43048
A;Accession: A43048
A;Molecule type: protein
A;Residues: 759-779 <RA2>
A;Experimental source: skin
C;Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hyd
C;Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) ar
C;Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine ski
9, 149, 268, and 217 residues.
C;Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
C;Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trime
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 3.7%; Score 9; DB 1; Length 779;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 PGRDGSPGA 71
|||||||||
Db 586 PGRDGSPGA 594

RESULT 5
JE0237
apolipoprotein E receptor 2 precursor - mouse
N;Alternate names: apoER2
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 18-Aug-2000
C;Accession: JE0237
R;Kim, H.J.; Kim, D.H.; Magoori, K.; Saeki, S.; Yamamoto, T.T.
J. Biochem. 124, 451-456, 1998
A;Title: Evolution of the apolipoprotein E receptor 2 gene by exon loss.
A;Reference number: JE0237; MUID:98352008; PMID:9685741
A;Accession: JE0237
A;Molecule type: mRNA
A;Residues: 1-996 <KIM>
A;Cross-references: DDBJ:D85463
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C;Keywords: glycoprotein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-996/Product: apolipoprotein E receptor 2 #status predicted <MAT>
F;41-75/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;80-116/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;121-157/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;161-195/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;200-237/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;251-286/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;291-325/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;331-368/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;373-407/Domain: EGF homology <EGF>
F;585-628/Domain: LDL receptor YWTD-containing repeat homology <YWT>
F;723-767/Domain: EGF homology <EGF1>
F;858-881/Domain: transmembrane #status predicted <TTM>
F;805,840/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.7%; Score 9; DB 2; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         16 LLLLLLLQL 24
               |||||||||
Db         14 LLLLLLLQL 22
```

RESULT 6
CGHU1S
collagen alpha 1(I) chain precursor - human
N;Alternate names: procollagen alpha 1(I) chain
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 31-Dec-2000
C;Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11
5269; A29439; I53466; A02852; I37247
R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
Gene 67, 105-115, 1988
A;Title: Complete nucleotide sequence of the region encompassing the first twenty-five e
A;Reference number: I60114; MUID:88329734; PMID:2843432
A;Accession: I60114
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369,'L',371-589 <DAL>
A;Cross-references: GB:M20789; NID:g179593; PIDN:AAB59373.1; PID:g179594
R;Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock
Biochem. J. 253, 919-922, 1988
A;Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
A;Reference number: S01143; MUID:89025644; PMID:3178743
A;Accession: S01143
A;Molecule type: mRNA
A;Residues: 1-472 <TRO>
A;Cross-references: EMBL:X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NID
A;Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988
R;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Nature 310, 337-340, 1984
A;Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of
A;Reference number: A93335; MUID:84270697; PMID:6462220
A;Accession: A93335
A;Molecule type: DNA
A;Residues: 1-58,'Q',60-181 <CHU>
A;Cross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658
R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet,
J. Biol. Chem. 262, 15151-15157, 1987
A;Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene
A;Reference number: I55254; MUID:88033098; PMID:2822714
A;Accession: I55254
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-45 <ROS>
A;Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388
R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional contro
A;Reference number: A39943; MUID:88097389; PMID:3480516
A;Accession: A39943
A;Molecule type: DNA
A;Residues: 1-34 <BOR>
A;Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238
R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promote
A;Reference number: I55237; MUID:85130970; PMID:2857713
A;Accession: I55237
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-34 <CH2>
A;Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226
R;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Holl
J. Biol. Chem. 265, 6312-6317, 1990
A;Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-term
rome, type VII.
A;Reference number: A35233; MUID:90202908; PMID:2318855
A;Accession: A35233
A;Molecule type: protein
A;Residues: 33-52 <WIR>
A;Note: this propeptide fragment remained non-covalently bound to a defective, unclea
R;Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.
EMBO J. 8, 1705-1710, 1989
A;Title: A base substitution in the exon of a collagen gene causes alternative splici
A;Reference number: S09400; MUID:89356643; PMID:2767050
A;Accession: S09400
A;Molecule type: mRNA
A;Residues: 156-183 <WEI>
R;Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A;Title: Isolation and characterization of the cyanogen bromide peptides from the alp
A;Reference number: A90567; MUID:71038625; PMID:5529814
A;Contents: CNBr0-1, CNBr2, CNBr4, CNBr5
A;Accession: B90567
A;Molecule type: protein
A;Residues: 162-198,'Z',200-201,'Z',203-206,'Z',208-209,'Z',211-228,'B',230,'BB',233,
A;Experimental source: skin
A;Note: evidence for 170-allysine
R;Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller
Eur. J. Biochem. 192, 153-159, 1990
A;Title: A critical crosslink region in human-bone-derived collagen type I. Specific
A;Reference number: S11372; MUID:90382436; PMID:2169412
A;Accession: S11372
A;Molecule type: protein
A;Residues: 175-187;274-287,'P',289 <BAE>
A;Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R;Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonza
J. Biol. Chem. 266, 21827-21832, 1991
A;Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen ch
ooperative melting of intact type I collagen.
A;Reference number: I55342; MUID:92042092; PMID:1718984
A;Accession: I55342
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A;Residues: 258-268;1347-1357 <DEA>
A;Cross-references: GB:S67495; NID:g239007; PIDN:AAB20350.1; PID:g239008
A;Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A;Reference number: A92069; MUID:71001508; PMID:4319110
A;Accession: A92069
A;Molecule type: protein
A;Residues: 263-268 <MOR>
A;Experimental source: skin
A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
R;Labhard, M.E.; Hollister, D.W.
Matrix 10, 124-130, 1990
A;Title: Segmental amplification of the entire helical and telopeptide regions of the cI
A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Accession: S15989
A;Molecule type: mRNA
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
R;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N
Connect. Tissue Res. 29, 1-11, 1993
A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
A;Reference number: I52905; MUID:93339042; PMID:8339541
A;Accession: I52905
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 342-352,'C',354-359 <WI2>
A;Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
A;Note: mutant sequence from patient with osteogenesis imperfecta
R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-5223, 1983
A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha1
A;Reference number: A90476; MUID:84080385; PMID:6689127
A;Accession: A90476
A;Molecule type: mRNA
A;Residues: 425-1250,'X',1252-1328,'S',1330-1390,'X',1392-1464 <BER>
A;Cross-references: GB:K01228; NID:g180391; PIDN:AAA51995.1; PID:g180392
A;Note: sequence partially completed for missing nucleotides by A29439
R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A;Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type II
A;Reference number: A22161; MUID:85104934; PMID:2981843
A;Accession: A22161
A;Molecule type: DNA
A;Residues: 472-594,'R',596-607 <CH3>
A;Cross-references: GB:K03178; GB:K03179; NID:g179612; NID:g179613; PIDN:AAA51847.1; PID
A;Note: the authors translated the codon CGT for residue 595 as Pro
R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
.
A;Reference number: A35336; MUID:90252792; PMID:2339700
A;Accession: A35336
A;Molecule type: mRNA
A;Residues: 710-720,'E',722-737,'E',739-745 <WAL>
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the c
A;Reference number: I54365; MUID:95187161; PMID:7881420
A;Accession: I54365
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 746-766,'S',768-781 <FOR>
A;Cross-references: GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID:g1009094
R;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
A;Reference number: A47426; MUID:93352646; PMID:8349697
A;Accession: A47426
A;Molecule type: mRNA
A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different
A;Accession: B47426
A;Molecule type: mRNA
A;Residues: 1179-1464 <CH4>
A;Experimental source: normal dermal fibroblast culture
A;Accession: C47426
A;Molecule type: mRNA
A;Residues: 1179-1276,'H',1278-1464 <CH5>
A;Experimental source: fetal cell 86-237
A;Accession: D47426
A;Molecule type: mRNA
A;Residues: 1179-1336,1339-1464 <CH6>
A;Experimental source: fetal cell 86-146
A;Accession: E47426
A;Molecule type: mRNA
A;Residues: 1179-1387,'R',1389-1464 <CH7>
A;Experimental source: fetal cell 88-251
R;Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.;
J. Biol. Chem. 263, 14605-14607, 1988
A;Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptid
A;Reference number: I55269; MUID:89008319; PMID:3170557
A;Accession: I55269
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1187-1194,'C',1196-1220 <COH>
A;Cross-references: GB:M23213; NID:g340842; PIDN:AAB59363.1; PID:g499622
A;Note: mutant sequence from a patient with mild osteogenesis imperfecta
R;Maekelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
Nucleic Acids Res. 16, 349, 1988
A;Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.

Query Match 3.7%; Score 9; DB 1; Length 1464;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 PGRDGSPGA 71
|||||||||
Db 1024 PGRDGSPGA 1032

RESULT 7
A60111
sporozoite antigen - Eimeria tenella (fragment)
C;Species: Eimeria tenella
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 17-Jul-1994
C;Accession: A60111
R;Miller, G.A.; Bhogal, B.S.; McCandliss, R.; Strausberg, R.L.; Jessee, E.J.; Anderso
Infect. Immun. 57, 2014-2020, 1989
A;Title: Characterization and vaccine potential of a novel recombinant coccidial anti
A;Reference number: A60111; MUID:89277516; PMID:2659532
A;Accession: A60111
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <MIL>

Query Match 3.3%; Score 8; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLLQ 23
||||||||
Db 3 LLLLLLLQ 10

RESULT 8
UTHUB
lutropin beta chain precursor [validated] - human
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizi
C;Species: Homo sapiens (man)
C;Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
C;Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.

Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin ar
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37994
A;Status: preliminary; translated from GB/EMBL/DDBJ; not compared with conceptual transl
A;Molecule type: DNA
A;Residues: 1-141 <TAL>
A;Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
R;Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A;Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A;Reference number: I58013; MUID:92085985; PMID:1727547
A;Accession: I58013
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 72-73,'R',75-76 <WEI>
A;Cross-references: GB:S71273; NID:g240572; PIDN:AAD14960.1; PID:g4262812
A;Note: mutant sequence from patient with hypogonadism
R;Sairam, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A;Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
A;Reference number: A90604; MUID:76062547; PMID:1191677
A;Accession: A90604
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SAI>
R;Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A;Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A;Reference number: A92759; MUID:73090987; PMID:4685398
A;Accession: A92759
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SHO>
R;Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A;Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
A;Reference number: A91389; MUID:73221227; PMID:4719207
A;Contents: annotation; partial sequence
R;Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A;Reference number: A94466
A;Accession: A94466
A;Molecule type: protein
A;Residues: 21-38,'Q',40-46 <WAR>
A;Note: 28-Val, 33-Arg, and 35-Thr were also found
R;Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A;Reference number: A94552
A;Contents: annotation; binding site
C;Genetics:
A;Gene: GDB:LHB
A;Cross-references: GDB:119364; OMIM:152780
A;Map position: 19q13.3-19q13.3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta #status experimental <LTB>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GLLLLLL 22
|||||||
Db 6 GLLLLLL 13

RESULT 9
KTHUB
choriogonadotropin beta chain precursor [validated] - human
N;Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C;Accession: A93230; I69972; I55224; I55250; I70007; I70008; A92303; A92181; A92142;
R;Fiddes, J.C.; Goodman, H.M.
Nature 286, 684-687, 1980
A;Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolu
A;Reference number: A93230; MUID:81012134; PMID:6774259
A;Accession: A93230
A;Molecule type: mRNA
A;Residues: 1-165 <FID>
A;Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA96690.1; PI
R;Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A;Title: The beta subunit of human chorionic gonadotropin is encoded by multiple gene
A;Reference number: I55224; MUID:84008141; PMID:6194155
A;Accession: I69972
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-165 <POL>
A;Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A;Note: clone CG-beta-e
A;Accession: I55224
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23,'M',25-136,'A',138-165 <PO2>
A;Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
A;Note: clone CG-beta-a
R;Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A;Title: A map of the hCG beta-LH beta gene cluster.
A;Reference number: I55250; MUID:86195987; PMID:2422163
A;Accession: I55250
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO3>
A;Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
A;Note: CG-beta-3 gene
A;Accession: I70007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO4>
A;Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
A;Note: CG-beta-6 gene
A;Accession: I70008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RE5>
A;Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090
A;Note: CG-beta-7 gene
R;Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A;Title: The amino acid sequences of the prepeptides contained in the alpha and beta
A;Reference number: A92303; MUID:81117268; PMID:7462224
A;Accession: A92303
A;Molecule type: protein
A;Residues: 1-20 <BIR>
A;Note: the identity of the residue at position 19 could not be determined
R;Morgan, F.J.; Birken, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A;Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit a
A;Reference number: A92181; MUID:75211304; PMID:1150658
A;Accession: A92181
A;Molecule type: protein
A;Residues: 21-165 <MOR>
R;Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A;Reference number: A92142; MUID:74011267; PMID:4795659
A;Accession: A92142
A;Molecule type: protein
A;Residues: 21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP' <CAR>
R;Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 558-562, 1990
A;Title: The immunological characteristics of the enzymatic fragments of human chorio

A;Reference number: PC1016
A;Accession: PC1016
A;Molecule type: protein
A;Residues: 21-165 <SHI>
A;Note: article in Chinese with English abstract
R;Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
Endocrinology 123, 572-583, 1988
A;Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
A;Reference number: A61097; MUID:88254680; PMID:2454811
A;Accession: A61097
A;Molecule type: protein
A;Residues: 26-32,'X',34-49,'X',51-60;75-112 <BI2>
A;Note: this material from pregancy urine lacks sialic acid in its carbohydrate and has
R;Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A;Title: Characterisation of UGP and its relationship with beta-core fragment.
A;Reference number: A56873; MUID:93229246; PMID:8471426
A;Accession: B56873
A;Molecule type: protein
A;Residues: 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',78-91,'G',93-102 <KA
A;Experimental source: urine
A;Note: sequence modified after extraction from NCBI backbone
A;Note: this material was designated urinary gonadotrophin peptide (peak 2)
R;Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin,
Nature 369, 455-461, 1994
A;Title: Crystal structure of human chorionic gonadotropin.
A;Reference number: A44674; MUID:94261179; PMID:8202136
A;Contents: annotation; X-ray crystallography, 3.0 angstroms; correction of disulfide bo
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 21-165 <RES>
A;Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075
C;Genetics:
A;Gene: GDB:CGB
A;Cross-references: GDB:119055; OMIM:118860
A;Map position: 19q13.3-19q13.3
A;Introns: 5/3; 61/3
A;Note: the choriogonadotropin beta chain locus contains six genes (or pseudogenes)
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-165/Product: choriogonadotropin beta chain #status experimental <MAT>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status experimental
F;33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 3.3%; Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GLLLLLLL 22
||||||||
Db 6 GLLLLLLL 13

RESULT 10
T18321
hypothetical protein L7610.12 - Leishmania major
C;Species: Leishmania major
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T18321
R;Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18876
A;Accession: T18321
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-169 <OLI>
A;Cross-references: EMBL:AL034356; NID:e1371878; PIDN:CAA22247.1
C;Genetics:
A;Note: L7610.12

Query Match 3.3%; Score 8; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PAASPQRL 13
||||||||
Db 18 PAASPQRL 25

RESULT 11
S37749
collagen alpha 2(XIV) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C;Accession: S37749
R;Brown, J.C.; Golbik, R.; Mann, K.; Timpl, R.
submitted to the EMBL Data Library, October 1993
A;Description: Structure and stability of the triple helical domains of human collage
A;Reference number: S37749
A;Accession: S37749
A;Molecule type: protein
A;Residues: 1-177 <BRO>
C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
ed and subsequently O-glycosylated.
C;Genetics:
A;Gene: COL14A2
C;Complex: type XIV collagen may be a heterotrimer of alpha 1(XIV) chains and one alp
C;Function:
A;Description: structural component of extracellular fibrous polymer associated with
C;Superfamily: collagen alpha 1(XIV) chain; fibronectin type III repeat homology; von
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr
F;9,24,39,45,59,62,74,80,86,92,98,106,109,116,119,122,137,140/Modified site: 4-hydrox
F;12/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;18,143/Modified site: 5-hydroxylysine (Lys) #status experimental
F;18,27,143/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;27/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 3.3%; Score 8; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 PGRDGSPG 70
||||||||
Db 86 PGRDGSPG 93

RESULT 12
T35724
cobalt transport integral membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
C;Accession: T35724
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21548
A;Accession: T35724
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-249 <MUR>
A;Cross-references: EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCOEDB:SC7H1.29c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: cbiQ; SCOEDB:SC7H1.29c
C;Superfamily: cobalt transport protein Q homolog

Query Match 3.3%; Score 8; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          58 GPAGVPGR 65
               ||||||||
Db          54 GPAGVPGR 61


RESULT 13
I38427
4-1BB ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38427
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; F
Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.
A;Reference number: I38426; MUID:94374434; PMID:8088337
A;Accession: I38427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-254 <RES>
A;Cross-references: EMBL:U03398; NID:g571322; PIDN:AAA53134.1; PID:g571323

  Query Match             3.3%;  Score 8;  DB 2;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 GLLLLLLL 22
               ||||||||
Db          34 GLLLLLLL 41


RESULT 14
B60131
homeotic protein Xhox-7.1' - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999
C;Accession: B60131; S14514
R;Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
Development 111, 1179-1187, 1991
A;Title: Progressively restricted expression of a new homeobox-containing gene during Xe
A;Reference number: A60131; MUID:91347929; PMID:1679007
A;Accession: B60131
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-9,'P',11-291 <SUA>
A;Cross-references: EMBL:X58772
R;Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F.
submitted to the EMBL Data Library, December 1990
A;Reference number: S14513
A;Accession: S14514
A;Molecule type: mRNA
A;Residues: 1-291 <SUA2>
A;Cross-references: EMBL:X58772; NID:g64784; PIDN:CAA41573.1; PID:g64785
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;161-217/Domain: homeobox homology <HOX>

  Query Match             3.3%;  Score 8;  DB 2;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          16 LLLLLLLQ 23
               ||||||||
Db           6 LLLLLLLQ 13


RESULT 15
T24827
hypothetical protein T11B7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T24827
R;Gardner, A.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19940
A;Accession: T24827
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
A;Cross-references: EMBL:Z54237; PIDN:CAA90989.1; GSPDB:GN00022; CESP:T11B7.3
A;Experimental source: clone T11B7
C;Genetics:
A;Gene: CESP:T11B7.3
A;Map position: 4
A;Introns: 45/3; 111/1; 270/1
C;Superfamily: unassigned collagens

  Query Match             3.3%;  Score 8;  DB 2;  Length 296;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          78 PGIPGRDG 85
               ||||||||
Db         266 PGIPGRDG 273


Search completed: August 13, 2003, 13:41:08
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:28:47 ; Search time 23 Seconds
(without alignments)
496.847 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1289

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	3.7	120	1	GON2_HUMAN	O43555 homo sapien
2	9	3.7	133	1	YJZ3_YEAST	P47094 saccharomyc
3	9	3.7	779	1	CA11_BOVIN	P02453 bos taurus
4	9	3.7	813	1	CADM_RAT	Q63315 rattus norv
5	9	3.7	905	1	ATS8_MOUSE	P57110 mus musculu
6	9	3.7	1464	1	CA11_HUMAN	P02452 homo sapien
7	8	3.3	141	1	LSHB_HUMAN	P01229 homo sapien
8	8	3.3	165	1	CGHB_HUMAN	P01233 homo sapien
9	8	3.3	233	1	RS3_BUCAP	Q8k956 buchnera ap
10	8	3.3	246	1	MOG_MOUSE	Q61885 mus musculu
11	8	3.3	254	1	TNF9_HUMAN	P41273 homo sapien
12	8	3.3	291	1	HX7P_XENLA	P35993 xenopus lae
13	8	3.3	365	1	WNT6_HUMAN	Q9y6f9 homo sapien
14	8	3.3	424	1	GSA_AQUAE	O66998 aquifex aeo
15	8	3.3	457	1	CD4_MOUSE	P06332 mus musculu
16	8	3.3	487	1	CPS1_MOUSE	P03940 mus musculu
17	8	3.3	500	1	CAMA_MOUSE	P51942 mus musculu
18	8	3.3	636	1	CA13_RAT	P13941 rattus norv
19	8	3.3	652	1	CD93_HUMAN	Q9npy3 homo sapien
20	8	3.3	674	1	CA1A_CHICK	P08125 gallus gall
21	8	3.3	787	1	SMO_HUMAN	Q99835 homo sapien
22	8	3.3	809	1	NAH2_RABIT	P50482 oryctolagus
23	8	3.3	832	1	SM4B_HUMAN	Q9npr2 homo sapien
24	8	3.3	984	1	PKL2_HUMAN	Q16513 homo sapien
25	8	3.3	1019	1	CA26_HUMAN	P12110 homo sapien
26	8	3.3	1029	1	CA26_MOUSE	Q02788 mus musculu
27	8	3.3	1103	1	CYGD_HUMAN	Q02846 homo sapien
28	8	3.3	1108	1	CYGE_MOUSE	P52785 mus musculu
29	8	3.3	1108	1	CYGE_RAT	P51840 rattus norv
30	8	3.3	1266	1	NGCA_CHICK	Q03696 gallus gall
31	8	3.3	1278	1	NPC1_MOUSE	O35604 mus musculu
32	8	3.3	1355	1	CA21_RANCA	O42350 rana catesb
33	8	3.3	1388	1	CA1E_HUMAN	P39059 homo sapien
34	8	3.3	1460	1	CA11_CANFA	Q9xsj7 canis famil
35	8	3.3	1464	1	CA13_MOUSE	P08121 mus musculu
36	8	3.3	1466	1	CA13_HUMAN	P02461 homo sapien
37	8	3.3	1531	1	MRP1_HUMAN	P33527 homo sapien
38	8	3.3	1564	1	MRP2_RABIT	Q28689 oryctolagus
39	7	2.9	31	1	LPL_BUCRP	Q53017 buchnera ap
40	7	2.9	61	1	DNBI_BFDV	P13893 budgerigar
41	7	2.9	77	1	ENV_SMSAV	P03384 simian sarc
42	7	2.9	77	1	YF78_ARCFU	O28694 archaeoglob
43	7	2.9	84	1	HEPC_HUMAN	P81172 homo sapien
44	7	2.9	100	1	MI2B_RAT	Q10747 rattus norv
45	7	2.9	101	1	GRO_CRIGR	P09340 cricetulus

ALIGNMENTS

RESULT 1
GON2_HUMAN
ID GON2_HUMAN STANDARD; PRT; 120 AA.
AC O43555; Q9BYN9; Q9BYP0;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin II precursor [Contains: Gonadoliberin II (LH-RH II)
DE (Luteinizing hormone-releasing hormone II) (Gonadotropin-releasing
DE hormone II) (GnRH II) (Luliberin II); GnRH-associated peptide II].
GN GNRH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98081869; PubMed=9419371;
RA White R.B., Eisen J.A., Kasten T.L., Fernald R.D.;
RT "Second gene for gonadotropin-releasing hormone in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:305-309(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
CC THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING
CC HORMONES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:

```
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=1;
CC         IsoId=O43555-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O43555-2; Sequence=VSP_001825;
CC       Name=3;
CC         IsoId=O43555-3; Sequence=VSP_001826;
CC   -!- TISSUE SPECIFICITY: MIDBRAIN; EXPRESSED AT SIGNIFICANTLY HIGHER
CC       LEVELS OUTSIDE THE BRAIN (UP TO 30-FOLD), PARTICULARLY IN THE
CC       KIDNEY, BONE MARROW, AND PROSTATE.
CC   -!- SIMILARITY: Belongs to the GNRH family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF036329; AAC02980.1; -.
DR   EMBL; AF036330; AAC02981.1; -.
DR   EMBL; AL121905; CAC10338.1; -.
DR   EMBL; AL121905; CAC29100.1; -.
DR   EMBL; AL121905; CAC29101.1; -.
DR   Genew; HGNC:4420; GNRH2.
DR   MIM; 602352; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Cleavage on pair of basic residues; Hormone; Amidation; Signal;
KW   Alternative splicing; Pyrrolidone carboxylic acid.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    120       PROGONADOLIBERIN II.
FT   PEPTIDE     24     33       GONADOLIBERIN II.
FT   PEPTIDE     39    120       GNRH-ASSOCIATED PEPTIDE II.
FT   MOD_RES     24     24       PYRROLIDONE CARBOXYLIC ACID
FT                               (BY SIMILARITY).
FT   MOD_RES     33     33       AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT   VARSPLIC    52     59       Missing (in isoform 2).
FT                               /FTId=VSP_001825.
FT   VARSPLIC    52     58       Missing (in isoform 3).
FT                               /FTId=VSP_001826.
SQ   SEQUENCE   120 AA;  12917 MW;  D58CDA14B6D6FB8D CRC64;

  Query Match             3.7%;  Score 9;  DB 1;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 RGLLLLLLL 22
              |||||||||
Db          6 RGLLLLLLL 14


RESULT 2
YJZ3_YEAST
ID   YJZ3_YEAST     STANDARD;      PRT;   133 AA.
AC   P47094;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Hypothetical 15.3 kDa protein in MER2-BNA1 intergenic region.
GN   YJR023C OR J1470 OR YJR83.19.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / FY1679;
RA   de Haan M., Smits P.H.M., Grivell L.A.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 13-93 FROM N.A.
RX   MEDLINE=96109930; PubMed=8619316;
RA   Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytka J.,
RA   Sulicka J., Herbert C.J.;
RT   "The sequence of 24.3 kb from chromosome X reveals five complete open
RT   reading frames, all of which correspond to new genes, and a tandem
RT   insertion of a Ty1 transposon.";
RL   Yeast 11:1179-1186(1995).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X87611; CAA60946.1; -.
DR   EMBL; Z49522; CAA89548.1; -.
DR   PIR; S57038; S57038.
DR   SGD; S0003784; YJR023C.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     8     28       POTENTIAL.
FT   TRANSMEM    46     66       POTENTIAL.
FT   DOMAIN      10     30       POLY-LEU.
FT   CONFLICT    28     28       MISSING (IN REF. 1).
SQ   SEQUENCE   133 AA;  15282 MW;  4303172FF2500008 CRC64;

  Query Match             3.7%;  Score 9;  DB 1;  Length 133;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         22 LLLLLLLQL 30


RESULT 3
CA11_BOVIN
ID   CA11_BOVIN     STANDARD;      PRT;   779 AA.
AC   P02453;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 1(I) chain (Fragments).
GN   COL1A1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE OF 1-19.
RX   MEDLINE=72255334; PubMed=4115172;
RA   Rauterberg J., Timpl R., Furthmayr H.;
RT   "Structural characterization of N-terminal antigenic determinants in
RT   calf and human collagen.";
RL   Eur. J. Biochem. 27:231-237(1972).
RN   [2]
RP   SEQUENCE OF 20-145.
RX   MEDLINE=76022320; PubMed=1164916;
RA   Fietzek P.P., Kuehn K.;
RT   "The covalent structure of collagen: amino-acid sequence of the
RT   cyanogen-bromide peptides alpha-1-CB2, alpha-1-CB4 and alpha-1-CB5
RT   from calf-skin collagen.";
RL   Eur. J. Biochem. 52:77-82(1975).
RN   [3]
RP   SEQUENCE OF 146-294.
```

```
RX   MEDLINE=73049499; PubMed=4673951;
RA   Fietzek P.P., Wendt P., Kell I., Kuehn K.;
RT   "The covalent structure of collagen: amino acid sequence of alpha-1-
RT   CB3 from calf skin collagen.";
RL   FEBS Lett. 26:74-76(1972).
RN   [4]
RP   SEQUENCE OF 295-562.
RX   MEDLINE=74086118; PubMed=4359390;
RA   Fietzek P.P., Rexrodt F.W., Hopper K.E., Kuehn K.;
RT   "The covalent structure of collagen. 2. The amino-acid sequence of
RT   alpha-1-CB7 from calf-skin collagen.";
RL   Eur. J. Biochem. 38:396-400(1973).
RN   [5]
RP   SEQUENCE OF 563-675.
RX   MEDLINE=73042276; PubMed=4343808;
RA   Wendt P., Mark K.V.D., Rexrodt F., Kuehn K.;
RT   "The covalent structure of collagen. The amino-acid sequence of the
RT   112-residues. Amino-terminal part of peptide alpha-1-CB6 from calf-
RT   skin collagen.";
RL   Eur. J. Biochem. 30:169-183(1972).
RN   [6]
RP   SEQUENCE OF 676-751.
RX   MEDLINE=73042275; PubMed=4343807;
RA   Fietzek P.P., Rexrodt F.W., Wendt P., Stark M., Kuehn K.;
RT   "The covalent structure of collagen. Amino-acid sequence of peptide
RT   alpha-1-CB6-C2.";
RL   Eur. J. Biochem. 30:163-168(1972).
CC   -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
CC       (FIBRILLAR FORMING COLLAGEN).
CC   -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
CC   -!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
CC       BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
CC       HYDROXYAPATITE.
CC   -!- PTM: Proline residues at the third position of the tripeptide
CC       repeating unit (G-X-Y) are hydroxylated in some or all of the
CC       chains. Pro-726 is the only 3-hydroxypro and the only hydroxylated
CC       proline in position X.
CC   -!- PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to
CC       the oxygen atom of a post-translationally added hydroxyl group.
CC   -!- MISCELLANEOUS: THE COMPLETE CHAIN CONTAINS 1052 RESIDUES.
DR   PIR; A91193; CGBO1S.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001007; VWF_C.
DR   ProDom; PD000007; Clg_helix; 1.
DR   PROSITE; PS01208; VWFC_1; PARTIAL.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Glycoprotein; Collagen; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       9      9       CONVERTED TO AN ALDEHYDE GROUP THAT IS
FT                                INVOLVED IN CROSS-LINKING.
FT   MOD_RES     103    103       HYDROXYLATION.
FT   CARBOHYD    103    103       O-LINKED (GAL. . .).
FT   MOD_RES     115    115       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     124    124       HYDROXYLATION (POTENTIAL).
FT   NON_CONS    145    146
FT   MOD_RES     274    274       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     346    346       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     424    424       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     496    496       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     658    658       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     670    670       HYDROXYLATION (POTENTIAL).
FT   MOD_RES     726    726       HYDROXYLATION.
SQ   SEQUENCE   779 AA;  70346 MW;  E554A7FF084283D1 CRC64;

  Query Match             3.7%;  Score 9;  DB 1;  Length 779;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        586 PGRDGSPGA 594
```

```
RESULT 4
CADM_RAT
ID   CADM_RAT       STANDARD;      PRT;   813 AA.
AC   Q63315; Q63561;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cadherin-22 precursor (PB-cadherin).
GN   CDH22.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RC   STRAIN=Wistar; TISSUE=Brain, and Pituitary;
RX   MEDLINE=96212232; PubMed=8626716;
RA   Sugimoto K., Honda S., Yamamoto T., Ueki T., Monden M., Kaji A.,
RA   Matsumoto K., Nakamura T.;
RT   "Molecular cloning and characterization of a newly identified member
RT   of the cadherin family, PB-cadherin.";
RL   J. Biol. Chem. 271:11548-11556(1996).
CC   -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC       They preferentially interact with themselves in a homophilic
CC       manner in connecting cells; cadherins may thus contribute to the
CC       sorting of heterogeneous cell types. PB-cadherins may have a role
CC       in the morphological organization of pituitary gland and brain
CC       tissues.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q63315-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q63315-2; Sequence=VSP_000643, VSP_000644;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and
CC       the brain (in the inner granular and glomerular layers of the
CC       olfactory bulb, anterior olfactory nucleus, primary olfactory
CC       cortex, Purkinje cell layer of cerebellum, and pineal gland). Low
CC       expression in lung and heart. No expression in submandibular
CC       gland, thymus, liver, spleen, adrenal, and kidney.
CC   -!- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.
CC   -!- SIMILARITY: Contains 5 cadherin domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D83348; BAA11894.1; -.
DR   EMBL; D83349; BAA11895.1; -.
DR   HSSP; P15116; 1NCJ.
DR   InterPro; IPR002126; Cadherin.
DR   InterPro; IPR000233; Cadherin_C_term.
DR   Pfam; PF00028; cadherin; 5.
DR   Pfam; PF01049; Cadherin_C_term; 1.
DR   PRINTS; PR00205; CADHERIN.
DR   SMART; SM00112; CA; 5.
DR   PROSITE; PS00232; CADHERIN_1; 2.
DR   PROSITE; PS50268; CADHERIN_2; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW   Signal; Alternative splicing.
FT   SIGNAL        1     33       POTENTIAL.
FT   CHAIN        34    813       CADHERIN-22.
FT   DOMAIN       33    621       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    622    642       POTENTIAL.
FT   DOMAIN      643    813       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       61    165       CADHERIN 1.
FT   DOMAIN      166    274       CADHERIN 2.
```

```
FT   DOMAIN       275     391       CADHERIN 3.
FT   DOMAIN       392     495       CADHERIN 4.
FT   DOMAIN       496     613       CADHERIN 5.
FT   CARBOHYD     159     159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     463     463       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     609     609       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     668     694       NDEGGGEQDTEAYDMSALRSLYDFGEL -> TLGSGHRGTS
FT                                  NKEDHQCPASLSLGFKP (in isoform 2).
FT                                  /FTId=VSP_000643.
FT   VARSPLIC     695     813       Missing (in isoform 2).
FT                                  /FTId=VSP_000644.
SQ   SEQUENCE   813 AA;  87978 MW;  30BEA60B5D2D467B CRC64;

  Query Match             3.7%;  Score 9;  DB 1;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         19 LLLLLLLQL 27


RESULT 5
ATS8_MOUSE
ID   ATS8_MOUSE      STANDARD;      PRT;   905 AA.
AC   P57110;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   ADAMTS-8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE   with thrombospondin motifs 8) (ADAM-TS 8) (ADAM-TS8) (METH-2).
GN   ADAMTS8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20079168; PubMed=10610729;
RA   Georgiadis K.E., Hirohata S., Seldin M.F., Apte S.S.;
RT   "ADAM-TS8, a novel metalloprotease of the ADAM-TS family located on
RT   mouse chromosome 9 and human chromosome 11.";
RL   Genomics 62:312-315(1999).
CC   -!- FUNCTION: HAS ANTI-ANGIOGENIC PROPERTIES (BY SIMILARITY).
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC       matrix (By similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN ADULT LUNG AND HEART
CC       AND LOW EXPRESSION DURING MOUSE DEVELOPMENT.
CC   -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
CC       FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
CC   -!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: Belongs to peptidase family M12B.
CC   -!- SIMILARITY: Contains 1 disintegrin-like domain.
CC   -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF175282; AAF25805.1; -.
DR   HSSP; P34179; 1IAG.
DR   MEROPS; M12.226; -.
DR   MGD; MGI:1353468; Adamts8.
DR   InterPro; IPR001762; Disintegrin.
DR   InterPro; IPR001590; Reprolysin.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR006025; Zn_MTpeptdse.
DR   Pfam; PF01421; Reprolysin; 1.
DR   Pfam; PF00090; tsp_1; 2.
DR   SMART; SM00209; TSP1; 2.
DR   PROSITE; PS50215; ADAM_MEPRO; 1.
DR   PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR   PROSITE; PS50214; DISINTEGRIN_2; FALSE_NEG.
DR   PROSITE; PS50092; TSP1; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
KW   Repeat; Extracellular matrix; Heparin-binding.
FT   SIGNAL         1     28       POTENTIAL.
FT   PROPEP        29     228      BY SIMILARITY.
FT   CHAIN        229     905      ADAMTS-8.
FT   DOMAIN       229     452      METALLOPROTEASE.
FT   DOMAIN       453     541      DISINTEGRIN-LIKE.
FT   DOMAIN       542     597      TSP TYPE-1 1.
FT   DOMAIN       599     705      CYS-RICH.
FT   DOMAIN       706     847      SPACER.
FT   DOMAIN       848     904      TSP TYPE-1 2.
FT   METAL        378     378      ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE     379     379      BY SIMILARITY.
FT   METAL        382     382      ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL        388     388      ZINC (CATALYTIC) (BY SIMILARITY).
FT   CARBOHYD     415     415      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     480     480      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     506     506      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     615     615      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   905 AA;  98879 MW;  124D4132B33A0CAE CRC64;

  Query Match             3.7%;  Score 9;  DB 1;  Length 905;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLLQLP 25
              |||||||||
Db         13 LLLLLLQLP 21


RESULT 6
CA11_HUMAN
ID   CA11_HUMAN      STANDARD;      PRT;  1464 AA.
AC   P02452; Q14037; Q15176;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Collagen alpha 1(I) chain precursor.
GN   COL1A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-472 FROM N.A.
RX   MEDLINE=89025644; PubMed=3178743;
RA   Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
RA   Jaenisch R., Prockup D.J.;
RT   "Structure of a full-length cDNA clone for the prepro alpha 1(I)
RT   chain of human type I procollagen.";
RL   Biochem. J. 253:919-922(1988).
RN   [2]
RP   SEQUENCE OF 1-181 FROM N.A.
RX   MEDLINE=84270697; PubMed=6462220;
RA   Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
RA   Myers J., Williams C., Ramirez F.;
RT   "Human pro alpha 1(I) collagen gene structure reveals evolutionary
RT   conservation of a pattern of introns and exons.";
RL   Nature 310:337-340(1984).
RN   [3]
RP   SEQUENCE OF 162-301.
RC   TISSUE=Skin;
RX   MEDLINE=71038625; PubMed=5529814;
RA   Click E.M., Bornstein P.;
RT   "Isolation and characterization of the cyanogen bromide peptides from
```

RT the alpha 1 and alpha 2 chains of human skin collagen.";
RL Biochemistry 9:4699-4706(1970).
RN [4]
RP SEQUENCE OF 263-268.
RC TISSUE=Skin;
RX MEDLINE=71001508; PubMed=4319110;
RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
RT "A comparative study of glycopeptides derived from selected
RT vertebrate collagens. A possible role of the carbohydrate in fibril
RT formation.";
RL J. Biol. Chem. 245:5042-5048(1970).
RN [5]
RP SEQUENCE OF 425-1464 FROM N.A.
RX MEDLINE=84080385; PubMed=6689127;
RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
RA Prockop D.J.;
RT "Nucleotide sequences of complementary deoxyribonucleic acids for the
RT pro alpha 1 chain of human type I procollagen. Statistical evaluation
RT of structures that are conserved during evolution.";
RL Biochemistry 22:5213-5223(1983).
RN [6]
RP SEQUENCE OF 1229-1454 FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=88124208; PubMed=3340531;
RA Maekelae J.K., Raassina M., Virta A., Vuorio E.;
RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
RT domain.";
RL Nucleic Acids Res. 16:349-349(1988).
RN [7]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=88097389; PubMed=3480516;
RA Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
RT "Regulatory elements in the first intron contribute to
RT transcriptional control of the human alpha 1(I) collagen gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
RN [8]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=85130970; PubMed=2857713;
RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
RT Promoter structure, AluI repeats, and polymorphic transcripts.";
RL J. Biol. Chem. 260:2315-2320(1985).
RN [9]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=88033098; PubMed=2822714;
RA Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
RA de Wet W.J.;
RT "DNA sequences in the first intron of the human pro-alpha 1(I)
RT collagen gene enhance transcription.";
RL J. Biol. Chem. 262:15151-15157(1987).
RN [10]
RP REVIEW ON VARIANTS.
RX MEDLINE=91184577; PubMed=2010058;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in collagen genes: causes of rare and some common diseases
RT in humans.";
RL FASEB J. 5:2052-2060(1991).
RN [11]
RP REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=9101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [12]
RP REVIEW ON OI VARIANTS.
RX MEDLINE=91374476; PubMed=1895312;
RA Byers P.H., Wallis G.A., Willing M.C.;
RT "Osteogenesis imperfecta: translation of mutation to phenotype.";
RL J. Med. Genet. 28:433-442(1991).
RN [13]
RP REVIEW ON OI VARIANTS.
RX MEDLINE=97169389; PubMed=9016532;
RA Dalgleish R.;
RT "The human type I collagen mutation database.";
RL Nucleic Acids Res. 25:181-187(1997).
RN [14]
RP VARIANT OI-II CYS-1166.
RX MEDLINE=86287390; PubMed=3016737;
RA Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
RT "Lethal osteogenesis imperfecta resulting from a single nucleotide
RT change in one human pro alpha 1(I) collagen allele.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
RN [15]
RP VARIANT OI-II ARG-569.
RX MEDLINE=87222295; PubMed=3108247;
RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
RT "Lethal perinatal osteogenesis imperfecta due to the substitution of
RT arginine for glycine at residue 391 of the alpha 1(I) chain of type I
RT collagen.";
RL J. Biol. Chem. 262:7021-7027(1987).
RN [16]
RP VARIANT OI-II CYS-926.
RX MEDLINE=88033031; PubMed=3667599;
RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
RT "A point mutation in a type I procollagen gene converts glycine 748
RT of the alpha 1 chain to cysteine and destabilizes the triple helix in
RT a lethal variant of osteogenesis imperfecta.";
RL J. Biol. Chem. 262:14737-14744(1987).
RN [17]
RP VARIANT OI-II ARG-842.
RX MEDLINE=88298828; PubMed=3403550;
RA Bateman J.F., Lamande S.R., Dahl H.H., Chan D., Cole W.G.;
RT "Substitution of arginine for glycine 664 in the collagen alpha 1(I)
RT chain in lethal perinatal osteogenesis imperfecta. Demonstration of
RT the peptide defect by in vitro expression of the mutant cDNA.";
RL J. Biol. Chem. 263:11627-11630(1988).
RN [18]
RP VARIANT OI CYS-1195.
RX MEDLINE=89218628; PubMed=3244312;
RA Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
RT "A cysteine for glycine substitution at position 1017 in an alpha
RT 1(I) chain of type I collagen in a patient with mild dominantly
RT inherited osteogenesis imperfecta.";
RL Mol. Biol. Med. 5:197-207(1988).
RN [19]
RP VARIANT OI-II VAL-434.
RX MEDLINE=89255493; PubMed=2470760;
RA Patterson E., Smiley E., Bonadio J.;
RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
RT mutation.";
RL J. Biol. Chem. 264:10083-10087(1989).
RN [20]
RP VARIANT OI-IV SER-1010.
RX MEDLINE=89308591; PubMed=2745420;
RA Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koeplin D.A.;
RT "Osteogenesis imperfecta type IV. Detection of a point mutation in
RT one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";
RL J. Biol. Chem. 264:11893-11900(1989).
RN [21]
RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
RX MEDLINE=89380165; PubMed=2777764;
RA Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
RT "Characterization of point mutations in the collagen COL1A1 and
RT COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";
RL J. Biol. Chem. 264:15809-15812(1989).
RN [22]
RP VARIANT OI SER-1022.
RX MEDLINE=90062068; PubMed=2511192;
RA Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe
RT variant of osteogenesis imperfecta minimally destabilizes the triple
RT helix of type I procollagen. The effects of glycine substitutions on
RT thermal stability are either position of amino acid specific.";
RL J. Biol. Chem. 264:19694-19699(1989).

```
RN   [23]
RP   VARIANT OI-II CYS-1082.
RX   MEDLINE=89109573; PubMed=2913053;
RA   Constantinou C.D., Nielsen K.B., Prockop D.J.;
RT   "A lethal variant of osteogenesis imperfecta has a single base
RT   mutation that substitutes cysteine for glycine 904 of the alpha 1(I)
RT   chain of type I procollagen. The asymptomatic mother has an
RT   unidentified mutation producing an overmodified and unstable type I
RT   procollagen.";
RL   J. Clin. Invest. 83:574-584(1989).
RN   [24]
RP   VARIANTS OI CYS-272; CYS-704 AND CYS-896.
RX   MEDLINE=90009313; PubMed=2794057;
RA   Starman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,
RA   Weiss L., Graham J.M., Byers P.H.;
RT   "Osteogenesis imperfecta. The position of substitution for glycine by
RT   cysteine in the triple helical domain of the pro alpha 1(I) chains of
RT   type I collagen determines the clinical phenotype.";
RL   J. Clin. Invest. 84:1206-1214(1989).
RN   [25]
RP   VARIANT OI-II CYS-422.

  Query Match             3.7%;  Score 9;  DB 1;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1024 PGRDGSPGA 1032


RESULT 7
LSHB_HUMAN
ID   LSHB_HUMAN      STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093590; PubMed=6690982;
RA   Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT   "Evolution of the genes for the beta subunits of human chorionic
RT   gonadotropin and luteinizing hormone.";
RL   Nature 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE=76062547; PubMed=1191677;
RA   Sairam M.R., Li C.H.;
RT   "Human pituitary lutropin. Isolation, properties, and the complete
RT   amino acid sequence of the beta-subunit.";
RL   Biochim. Biophys. Acta 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE=73090987; PubMed=4685398;
RA   Shome B., Parlow A.F.;
RT   "The primary structure of the hormone-specific, beta subunit of human
RT   pituitary luteinizing hormone (hLH).";
RL   J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE=73221227; PubMed=4719207;
RA   Closset J., Hennen G., Lequin R.M.;
RT   "Human luteinizing hormone. The amino acid sequence of the
RT   subunit.";
RL   FEBS Lett. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE=91122088; PubMed=1991473;
RA   Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT   "NMR investigations of the N-linked oligosaccharides at individual
RT   glycosylation sites of human lutropin.";
RL   Eur. J. Biochem. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE=92357029; PubMed=1495492;
RA   Keutmann H.T., Hua Q.-X., Weiss M.A.;
RT   "Structure of a receptor-binding fragment from human luteinizing
RT   hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT   resonance spectroscopy.";
RL   Mol. Endocrinol. 6:904-913(1992).
RN   [7]
RP   VARIANT HYPOGONADISM ARG-74.
RX   MEDLINE=92085985; PubMed=1727547;
RA   Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RA   Jameson J.L.;
RT   "Hypogonadism caused by a single amino acid substitution in the beta
RT   subunit of luteinizing hormone.";
RL   New Engl. J. Med. 326:179-183(1992).
RN   [8]
RP   VARIANT SER-122.
RX   PubMed=9457942;
RA   Liao W.X., Roy A.C., Chan C., Arulkumaran S., Ratnam S.S.;
RT   "A new molecular variant of luteinizing hormone associated with female
RT   infertility.";
RL   Fertil. Steril. 69:102-106(1998).
RN   [9]
RP   VARIANTS ARG-28 AND THR-35.
RX   PubMed=9886510;
RA   Takahashi K., Kurioka H., Ozaki T., Kanasaki H., Kohsaka M.,
RA   Miyazaki K., Karino K.;
RT   "Increased prevalence of luteinizing hormone beta-subunit variant in
RT   Japanese infertility patients.";
RL   Hum. Reprod. 13:3338-3344(1998).
RN   [10]
RP   VARIANT THR-18.
RX   PubMed=11870227;
RA   Jiang M., Lamminen T., Pakarinen P., Hellman J., Manna P.,
RA   Herrera R.J., Huhtaniemi I.;
RT   "A novel Ala(-3)Thr mutation in the signal peptide of human
RT   luteinizing hormone beta-subunit: potentiation of the inositol
RT   phosphate signalling pathway and attenuation of the adenylate cyclase
RT   pathway by recombinant variant hormone.";
RL   Mol. Hum. Reprod. 8:201-212(2002).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: Defects in LHB are a cause of hypogonadism [MIM:152780]
CC       which is characterized by infertility and pseudohermaphroditism.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00264; CAA25067.1; -.
DR   EMBL; S71273; AAD14960.1; ALT_SEQ.
DR   PIR; I37994; UTHUB.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P01229; -.
DR   Genew; HGNC:6584; LHB.
```

```
DR   MIM; 152780; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0008584; P:male gonad development; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
KW   Disease mutation; Polymorphism.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000045.
FT   VARIANT      18     18       A -> T (more effective in stimulating IP3
FT                                but not cAMP production).
FT                                /FTId=VAR_015672.
FT   VARIANT      28     28       W -> R (in dbSNP:1800447).
FT                                /FTId=VAR_014589.
FT   VARIANT      35     35       I -> T (in dbSNP:1800448).
FT                                /FTId=VAR_014590.
FT   VARIANT      74     74       Q -> R (in hypogonadism; lack of
FT                                receptor-binding).
FT                                /FTId=VAR_003189.
FT   VARIANT     122    122       G -> S (may be implicated in female
FT                                infertility).
FT                                /FTId=VAR_015673.
FT   CONFLICT     39     39       E -> Q (IN REF. 2).
FT   CONFLICT     76     76       MISSING (IN REF. 2).
FT   CONFLICT    132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  E411766253113F7C CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 141;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GLLLLLL 22
              |||||||
Db          6 GLLLLLL 13


RESULT 8
CGHB_HUMAN
ID   CGHB_HUMAN     STANDARD;      PRT;   165 AA.
AC   P01233; Q13991; Q14000; Q8WTT5; Q8WXL2; Q8WXL3; Q8WXL4;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE   subunit) (CG-beta).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81012134; PubMed=6774259;
RA   Fiddes J.C., Goodman H.M.;
RT   "The cDNA for the beta-subunit of human chorionic gonadotropin
RT   suggests evolution of a gene by readthrough into the 3'-untranslated
RT   region.";
RL   Nature 286:684-687(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093590; PubMed=6690982;
RA   Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT   "Evolution of the genes for the beta subunits of human chorionic
RT   gonadotropin and luteinizing hormone.";
RL   Nature 307:37-40(1984).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84008141; PubMed=6194155;
RA   Policastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R.,
RA   Boime I.;
RT   "The beta subunit of human chorionic gonadotropin is encoded by
RT   multiple genes.";
RL   J. Biol. Chem. 258:11492-11499(1983).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 6-164 FROM N.A., AND VARIANTS ALA-18; ARG-22; MET-24;
RP   TRP-28; HIS-30; ALA-137 AND CYS-147.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE OF 1-20.
RX   MEDLINE=81117268; PubMed=7462224;
RA   Birken S., Fetherston J., Canfield R.E., Boime I.;
RT   "The amino acid sequences of the prepeptides contained in the alpha
RT   and beta subunits of human choriogonadotropin.";
RL   J. Biol. Chem. 256:1816-1823(1981).
RN   [7]
RP   SEQUENCE OF 21-165.
RX   MEDLINE=75211304; PubMed=1150658;
RA   Morgan F.J., Birken S., Canfield R.E.;
RT   "The amino acid sequence of human chorionic gonadotropin. The alpha
RT   subunit and beta subunit.";
RL   J. Biol. Chem. 250:5247-5258(1975).
RN   [8]
RP   PRELIMINARY SEQUENCE OF 21-165.
RX   MEDLINE=74011267; PubMed=4795659;
RA   Carlsen R.B., Bahl O.P., Swaminathan N.;
RT   "Human chorionic gonadotropin. Linear amino acid sequence of the beta
RT   subunit.";
RL   J. Biol. Chem. 248:6810-6827(1973).
RN   [9]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE=86195987; PubMed=2422163;
RA   Policastro P.F., Daniels-Mcqueen S., Carle G., Boime I.;
RT   "A map of the hCG beta-LH beta gene cluster.";
```

```
RL   J. Biol. Chem. 261:5907-5916(1986).
RN   [10]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE=81215630; PubMed=7240231;
RA   Mise T., Bahl O.P.;
RT   "Assignment of disulfide bonds in the beta subunit of human chorionic
RT   gonadotropin.";
RL   J. Biol. Chem. 256:6587-6592(1981).
RN   [11]
RP   DISULFIDE BONDS.
RX   MEDLINE=90094415; PubMed=1688430;
RA   Saccuzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
RA   Ruddon R.W.;
RT   "Role of disulfide bond formation in the folding of human chorionic
RT   gonadotropin beta subunit into an alpha beta dimer assembly-competent
RT   form.";
RL   J. Biol. Chem. 265:312-317(1990).
RN   [12]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=92314469; PubMed=1820200;
RA   Weisshaar G., Hiyama J., Renwick A.G.C.;
RT   "Site-specific N-glycosylation of human chorionic gonadotrophin --
RT   structural analysis of glycopeptides by one- and two-dimensional 1H
RT   NMR spectroscopy.";
RL   Glycobiology 1:393-404(1991).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=94261179; PubMed=8202136;
RA   Lapthorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
RA   Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
RT   "Crystal structure of human chorionic gonadotropin.";
RL   Nature 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
CC   -!- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
CC       Profasi (Serono).
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00117; AAA96690.1; -.
DR   EMBL; X00265; CAA25068.1; ALT_INIT.
DR   EMBL; X00266; CAA25069.1; ALT_INIT.
DR   EMBL; M13504; AAA52005.1; -.
DR   EMBL; M13505; AAA52008.1; -.
DR   EMBL; M13503; AAA52009.1; -.
DR   EMBL; K03189; AAA53288.1; -.
DR   EMBL; K03187; AAA53288.1; JOINED.
DR   EMBL; K03188; AAA53288.1; JOINED.
DR   EMBL; K03183; AAA53287.1; -.
DR   EMBL; K00092; AAA53287.1; JOINED.
DR   EMBL; K03182; AAA53287.1; JOINED.
DR   EMBL; BC006290; AAH06290.1; -.
DR   EMBL; BC022796; AAH22796.1; -.
DR   EMBL; BC030994; AAH30994.1; -.
DR   EMBL; AF397576; AAL69704.1; -.
DR   EMBL; AF397577; AAL69705.1; -.
DR   EMBL; AF397578; AAL69706.1; -.
DR   EMBL; AF397579; AAL69707.1; -.
DR   EMBL; AF397580; AAL69708.1; -.
DR   PIR; A93230; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   PDB; 1QFW; 26-APR-00.
DR   PDB; 1XUL; 15-MAY-97.
DR   GlycoSuiteDB; P01233; -.
DR   Genew; HGNC:1886; CGB.
DR   Genew; HGNC:16451; CGB7.
DR   Genew; HGNC:16452; CGB5.
DR   MIM; 118860; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005179; F:hormone activity; TAS.
DR   GO; GO:0006915; P:apoptosis; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007292; P:oogenesis; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure;
KW   Polymorphism.
FT   SIGNAL       1     20
FT   CHAIN       21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID    29     77
FT   DISULFID    43     92
FT   DISULFID    46    130
FT   DISULFID    54    108
FT   DISULFID    58    110
FT   DISULFID   113    120
FT   CARBOHYD    33     33
FT                               N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000042.

  Query Match              3.3%;  Score 8;  DB 1;  Length 165;
  Best Local Similarity  100.0%;  Pred. No. 3.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GLLLLLLL 22
              ||||||||
Db          6 GLLLLLLL 13


RESULT 9
RS3_BUCAP
ID   RS3_BUCAP      STANDARD;      PRT;   233 AA.
AC   Q8K956;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   30S ribosomal protein S3.
GN   RPSC OR BUSG499.
OS   Buchnera aphidicola (subsp. Schizaphis graminum).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Buchnera.
OX   NCBI_TaxID=98794;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22084549; PubMed=12089438;
RA   Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA   Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT   "50 million years of genomic stasis in endosymbiotic bacteria.";
RL   Science 296:2376-2379(2002).
CC   -!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
CC       in the 70S ribosome, positioning it for translation (By
CC       similarity).
CC   -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
CC       with proteins S10 and S14 (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
CC   -!- SIMILARITY: Contains 1 KH type-2 domain.
CC   ---------------------------------------------------------------------
```

```
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE014125; AAM68042.1; -.
DR   HAMAP; MF_01309; -; 1.
DR   InterPro; IPR004087; KH_dom.
DR   InterPro; IPR004044; KH_TYPE_2.
DR   InterPro; IPR001351; Ribosomal_S3.
DR   InterPro; IPR005704; S3_bact.
DR   Pfam; PF00013; KH; 1.
DR   Pfam; PF00189; Ribosomal_S3_C; 1.
DR   Pfam; PF00417; Ribosomal_S3_N; 1.
DR   SMART; SM00322; KH; 1.
DR   TIGRFAMs; TIGR01009; rpsC_bact; 1.
DR   PROSITE; PS50823; KH_TYPE_2; 1.
DR   PROSITE; PS00548; RIBOSOMAL_S3; 1.
KW   Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
FT   DOMAIN       39    107       KH TYPE-2.
SQ   SEQUENCE   233 AA;  26530 MW;  60C476BEA7081BA5 CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 233;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        232 SVSRIIIE 239
              ||||||||
Db         51 SVSRIIIE 58


RESULT 10
MOG_MOUSE
ID   MOG_MOUSE      STANDARD;      PRT;   246 AA.
AC   Q61885; P70364; Q62003;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Myelin-oligodendrocyte glycoprotein precursor.
GN   MOG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=95130110; PubMed=7829100;
RA   Daubas P., Pham-Dinh D., Dautigny A.;
RT   "Structure and polymorphism of the mouse myelin/oligodendrocyte
RT   glycoprotein gene.";
RL   Genomics 23:36-41(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gardinier M.V., Matthieu J.M.;
RT   "Murine and human MOG are highly conserved: cDNA analysis.";
RL   Trans. Am. Soc. Neurochem. 24:234-234(1993).
RN   [3]
RP   SEQUENCE OF 29-246 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=93376728; PubMed=8367453;
RA   Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Roussel G.,
RA   Pontarotti P., Roeckel N., Mather I.H., Artzt K., Lindahl K.F.,
RA   Dautigny A.;
RT   "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
RT   immunoglobulin superfamily encoded within the major
RT   histocompatibility complex.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
RN   [4]
RP   SEQUENCE OF 29-54.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92218912; PubMed=1373175;
RA   Amiguet P., Gardinier M.V., Zanetta J.-P., Matthieu J.-M.;
RT   "Purification and partial structural and functional characterization
RT   of mouse myelin/oligodendrocyte glycoprotein.";
RL   J. Neurochem. 58:1676-1682(1992).
CC   -!- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC       COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC       CELL COMMUNICATION.
CC   -!- SUBUNIT: MAY FORM HOMODIMERS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC       LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC       MEMBRANES.
CC   -!- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND
CC       QUACKING DYSMYELINATING MUTANT MICE.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
CC       WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L29503; AAC42023.1; -.
DR   EMBL; L29498; AAC42023.1; JOINED.
DR   EMBL; L29500; AAC42023.1; JOINED.
DR   EMBL; L29501; AAC42023.1; JOINED.
DR   EMBL; L29499; AAC42023.1; JOINED.
DR   EMBL; L29502; AAC42023.1; JOINED.
DR   EMBL; U64572; AAB08096.1; -.
DR   EMBL; L20942; AAA03180.1; -.
DR   PIR; A55717; A55717.
DR   MGD; MGI:97435; Mog.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
FT   SIGNAL        1     28
FT   CHAIN        29    246       MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
FT   DOMAIN       29    156       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    157    177       POTENTIAL.
FT   DOMAIN      178    209       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    210    230       POTENTIAL.
FT   DOMAIN      231    246       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       31    144       IG-LIKE V-TYPE.
FT   DISULFID     52    126       POTENTIAL.
FT   CARBOHYD     59     59       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     21     21       L -> LL (IN REF. 2).
FT   CONFLICT     32     32       R -> G (IN REF. 4).
FT   CONFLICT     95     95       G -> E (IN REF. 3).
FT   CONFLICT    169    169       P -> S (IN REF. 2).
SQ   SEQUENCE   246 AA;  28271 MW;  1F1A8A4A0D5CFB89 CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 246;
  Best Local Similarity   100.0%;  Pred. No. 5.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLLQL 24
              ||||||||
Db         16 LLLLLLQL 23


RESULT 11
```

```
TNF9_HUMAN
ID   TNF9_HUMAN      STANDARD;      PRT;   254 AA.
AC   P41273;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 9 (4-1BB ligand) (4-
DE   1BBL).
GN   TNFSF9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94374434; PubMed=8088337;
RA   Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA   Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT   "Molecular and biological characterization of human 4-1BB and its
RT   ligand.";
RL   Eur. J. Immunol. 24:2219-2227(1994).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF9. Induces the
CC       proliferation of activated peripheral blood T cells. May have a
CC       role in activation-induced cell death (AICD). May play a role in
CC       cognate interactions between T cells and B cells/macrophages.
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL
CC       MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U03398; AAA53134.1; -.
DR   PIR; I38427; I38427.
DR   Genew; HGNC:11939; TNFSF9.
DR   MIM; 606182; -.
DR   GO; GO:0006915; P:apoptosis; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Polymorphism.
FT   DOMAIN        1     28       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      29    49       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN        50    254      EXTRACELLULAR (POTENTIAL).
FT   DOMAIN        35    41       POLY-LEU.
FT   VARIANT       17    17       P -> A (IN dbSNP:442511).
FT                                /FTId=VAR_011928.
SQ   SEQUENCE   254 AA;  26624 MW;  827551F34563E508 CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GLLLLLLL 22
              ||||||||
Db         34 GLLLLLLL 41


RESULT 12
HX7P_XENLA
ID   HX7P_XENLA      STANDARD;      PRT;   291 AA.
AC   P35993;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Homeobox protein XHOX-7.1' (Fragment).
GN   XHOX-7.1'.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91347929; PubMed=1679007;
RA   Su M.-W., Suzuki H.R., Solursh M., Ramirez F.;
RT   "Progressively restricted expression of a new homeobox-containing
RT   gene during Xenopus laevis embryogenesis.";
RL   Development 111:1179-1187(1991).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC   -!- SIMILARITY: BELONGS TO THE MSH HOMEOBOX FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X58772; CAA41573.1; -.
DR   PIR; B60131; B60131.
DR   HSSP; P22808; 1NK3.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR000047; HTH_lambrepressr.
DR   Pfam; PF00046; homeobox; 1.
DR   PRINTS; PR00024; HOMEOBOX.
DR   PRINTS; PR00031; HTHREPRESSR.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT   NON_TER       1     1
FT   DNA_BIND      160   219      HOMEOBOX.
SQ   SEQUENCE   291 AA;  32293 MW;  9D3D45FB6EF9CB50 CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQ 23
              ||||||||
Db          6 LLLLLLLQ 13


RESULT 13
WNT6_HUMAN
ID   WNT6_HUMAN      STANDARD;      PRT;   365 AA.
AC   Q9Y6F9; Q9H1J6; Q9H238;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Wnt-6 protein precursor.
GN   WNT6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y.,
RA   Kelsell D.P., Murdock P.R., Herrity N.C., Lewis C.J., Cross D.A.,
```

```
RA   Culbert A.A., Reith A.D., Barnes M.R.;
RT   "Molecular cloning and characterization of six novel human WNT
RT   genes.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21248387; PubMed=11350055;
RA   Kirikoshi H., Sekihara H., Katoh M.;
RT   "WNT10A and WNT6, clustered in human chromosome 2q35 region with
RT   head-to-tail manner, are strongly co-expressed in SW480 cells.";
RL   Biochem. Biophys. Res. Commun. 283:798-805(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buétow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 28-365 FROM N.A.
RA   Rump A., Hayes C., Brown S.D.M., Rosenthal A.;
RT   "Genomic sequence of the Wnt6 gene and the Wnt10a gene from human
RT   2q35.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 295-337 FROM N.A.
RX   MEDLINE=99276447; PubMed=10343101;
RA   Rankin J., Strachan T., Lako M., Lindsay S.;
RT   "Partial cloning and assignment of WNT6 to human chromosome band 2q35
RT   by in situ hybridization.";
RL   Cytogenet. Cell Genet. 84:50-52(1999).
CC   -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC       TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC       SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
CC       REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
CC       DIAMETERS.
CC   -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC       extracellular matrix.
CC   -!- SIMILARITY: Belongs to the Wnt family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY009401; AAG38661.1; -.
DR   EMBL; AB059570; BAB55603.1; -.
DR   EMBL; BC004329; AAH04329.1; -.
DR   EMBL; AF315943; AAG45154.1; -.
DR   EMBL; AF079522; AAD41674.1; -.
DR   PIR; JC7694; JC7694.
DR   Genew; HGNC:12785; WNT6.
DR   MIM; 604663; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR   GO; GO:0007267; P:cell-cell signaling; NAS.
DR   GO; GO:0007275; P:development; NAS.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
DR   PROSITE; PS00246; WNT1; 1.
KW   Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25    365       WNT-6 PROTEIN.
FT   CARBOHYD    86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   311    311       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   365 AA;  39720 MW;  928DE396C58E295B CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 365;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GLLLLLLL 22
              ||||||||
Db         10 GLLLLLLL 17


RESULT 14
GSA_AQUAE
ID   GSA_AQUAE      STANDARD;      PRT;   424 AA.
AC   O66998;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)
DE   (Glutamate-1-semialdehyde aminotransferase) (GSA-AT).
GN   HEML OR GSA OR AQ_816.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   -!- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
CC       aminolevulinate.
CC   -!- COFACTOR: Pyridoxal phosphate.
CC   -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; second step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC       aminotransferases.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000709; AAC06964.1; -.
DR   PIR; C70371; C70371.
DR   HSSP; P24630; 2GSA.
DR   HAMAP; MF_00375; -; 1.
DR   InterPro; IPR005814; Aminotrans_3.
DR   InterPro; IPR004639; HemL.
DR   Pfam; PF00202; aminotran_3; 1.
```

```
DR   TIGRFAMs; TIGR00713; hemL; 1.
DR   PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
KW   Porphyrin biosynthesis; Isomerase; Pyridoxal phosphate;
KW   Complete proteome.
FT   BINDING     264    264       PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ   SEQUENCE   424 AA;  46393 MW;  114DEF64E005E1E4 CRC64;

  Query Match              3.3%;  Score 8;  DB 1;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 8.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 IPGTPGIP 81
              ||||||||
Db        161 IPGTPGIP 168


RESULT 15
CD4_MOUSE
ID   CD4_MOUSE      STANDARD;      PRT;   457 AA.
AC   P06332;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE   T4/Leu-3) (T-cell differentiation antigen L3T4).
GN   CD4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87018845; PubMed=3094146;
RA   Tourvieille B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;
RT   "Isolation and sequence of L3T4 complementary DNA clones: expression
RT   in T cells and brain.";
RL   Science 234:610-614(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87115821; PubMed=3027575;
RA   Littman D.R., Gettner S.N.;
RT   "Unusual intron in the immunoglobulin domain of the newly isolated
RT   murine CD4 (L3T4) gene.";
RL   Nature 325:453-455(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88152875; PubMed=3326818;
RA   Parnes J.R., Hunkapiller T.;
RT   "L3T4 and the immunoglobulin gene superfamily: new relationships
RT   between the immune system and the nervous system.";
RL   Immunol. Rev. 100:109-127(1987).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RX   MEDLINE=88041159; PubMed=2823269;
RA   Gorman S.D., Tourvieille B., Parnes J.R.;
RT   "Structure of the mouse gene encoding CD4 and an unusual transcript
RT   in brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98112780; PubMed=9445485;
RA   Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
RA   Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
RA   Gibbs R.A.;
RT   "Comparative sequence analysis of a gene-rich cluster at human
RT   chromosome 12p13 and its syntenic region in mouse chromosome 6.";
RL   Genome Res. 8:29-40(1998).
RN   [6]
RP   SEQUENCE OF 27-43.
RX   MEDLINE=86166694; PubMed=3082751;
RA   Classon B.J., Tsagaratos J., Kirszbaum L., Maddox J., McKay C.R.,
RA   Brandon M., McKenzie I.F.C., Walker I.D.;
RT   "The L3T4 antigen in mouse and the sheep equivalent are
RT   immunoglobulin-like.";
RL   Immunogenetics 23:129-132(1986).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=86233454; PubMed=3086886;
RA   Classon B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
RT   "Partial primary structure of the T4 antigens of mouse and sheep:
RT   assignment of intrachain disulfide bonds.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
CC   -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC       RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC   -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P06332-1; Sequence=Displayed;
CC       Name=2; Synonyms=Brain-specific;
CC         IsoId=P06332-2; Sequence=VSP_002489;
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M36850; AAA39401.1; -.
DR   EMBL; M13816; AAA37267.1; -.
DR   EMBL; X04836; CAA28539.1; -.
DR   EMBL; M36851; AAA39402.1; -.
DR   EMBL; M17080; AAA37403.1; -.
DR   EMBL; M17078; AAA37403.1; JOINED.
DR   EMBL; M17079; AAA37403.1; JOINED.
DR   EMBL; AC002397; AAC36010.1; -.
DR   PIR; A02110; RWMST4.
DR   HSSP; P01730; 1WBR.
DR   MGD; MGI:88335; Cd4.
DR   GO; GO:0042101; C:T-cell receptor complex; ISS.
DR   GO; GO:0015026; F:coreceptor activity; ISS.
DR   GO; GO:0042289; F:MHC class II protein binding activity; ISS.
DR   GO; GO:0006955; P:immune response; ISS.
DR   GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR   GO; GO:0030217; P:T-cell differentiation; ISS.
DR   GO; GO:0045058; P:T-cell selection; ISS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR   InterPro; IPR000973; CD4_TCAg.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR00692; CD4TCANTIGEN.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW   Immune response; Repeat; Signal; Lipoprotein; Palmitate;
KW   Alternative splicing.
FT   SIGNAL       1     26
FT   CHAIN       27    457       T-CELL SURFACE GLYCOPROTEIN CD4.
FT   DOMAIN      27    394       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   395    417       POTENTIAL.
FT   DOMAIN     418    457       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      27    128       IG-LIKE V-TYPE.
FT   DOMAIN     129    207       IG-LIKE C2-TYPE 1.
FT   DOMAIN     208    317       IG-LIKE C2-TYPE 2.
FT   DOMAIN     318    374       IG-LIKE C2-TYPE 3.
FT   CARBOHYD   187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   298    298       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT   CARBOHYD     323     323       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     392     392       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID      42     112
FT   DISULFID     159     188
FT   DISULFID     328     370
FT   LIPID        418     418       PALMITATE (BY SIMILARITY).
FT   LIPID        421     421       PALMITATE (BY SIMILARITY).
FT   VARSPLIC       1     240       Missing (in isoform 2).
FT                                  /FTId=VSP_002489.
SQ   SEQUENCE   457 AA;  51296 MW;  1B1DA7527CB00F33 CRC64;

  Query Match             3.3%;  Score 8;  DB 1;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLLQL 24
              ||||||||
Db         10 LLLLLLQL 17


Search completed: August 13, 2003, 13:38:39
Job time : 25 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:35:12 ; Search time 96 Seconds
(without alignments)
653.196 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 6

Total number of hits satisfying chosen parameters: 5107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	70.0	243	4	Q96CG8	Q96cg8 homo sapien
2	169	69.5	232	4	Q8IX63	Q8ix63 homo sapien
3	111	45.7	245	11	Q9D1D6	Q9d1d6 mus musculu
4	111	45.7	245	11	Q8CG08	Q8cg08 rattus norv
5	9	3.7	41	4	Q9UMM7	Q9umm7 homo sapien
6	9	3.7	144	5	P90741	P90741 caenorhabdi
7	9	3.7	501	10	Q9AVM0	Q9avm0 asparagus o
8	9	3.7	558	10	Q9ASN8	Q9asn8 oryza sativ
9	9	3.7	870	11	Q921B6	Q921b6 mus musculu
10	9	3.7	996	11	Q924X6	Q924x6 mus musculu
11	9	3.7	1461	4	O76045	O76045 homo sapien
12	9	3.7	1464	4	Q8N473	Q8n473 homo sapien
13	8	3.3	59	11	Q8K3I2	Q8k3i2 mus musculu
14	8	3.3	65	11	Q91ZH3	Q91zh3 mus musculu
15	8	3.3	108	11	Q9D9P8	Q9d9p8 mus musculu
16	8	3.3	111	5	Q9W2P6	Q9w2p6 drosophila
17	8	3.3	113	11	Q60810	Q60810 mus musculu
18	8	3.3	116	5	Q8T3M4	Q8t3m4 drosophila
19	8	3.3	125	5	Q8IR67	Q8ir67 drosophila
20	8	3.3	136	4	Q8WXL0	Q8wxl0 homo sapien
21	8	3.3	141	6	Q9XSE0	Q9xse0 bos taurus
22	8	3.3	159	4	Q8WXL1	Q8wxl1 homo sapien
23	8	3.3	181	16	Q8D4M9	Q8d4m9 vibrio vuln
24	8	3.3	185	11	Q9JL41	Q9jl41 mus musculu
25	8	3.3	204	11	Q8CGL2	Q8cgl2 rattus norv
26	8	3.3	228	4	Q8IXU9	Q8ixu9 homo sapien
27	8	3.3	230	11	Q9R149	Q9r149 cavia porce
28	8	3.3	249	16	O54188	O54188 streptomyce
29	8	3.3	249	17	Q8U2U7	Q8u2u7 pyrococcus
30	8	3.3	251	4	Q8WY22	Q8wy22 homo sapien
31	8	3.3	259	4	Q8NBH9	Q8nbh9 homo sapien
32	8	3.3	272	16	Q8D1L1	Q8d1l1 yersinia pe
33	8	3.3	284	4	Q9UC14	Q9uc14 homo sapien
34	8	3.3	289	4	Q96A28	Q96a28 homo sapien
35	8	3.3	290	10	Q9XH03	Q9xh03 arabidopsis
36	8	3.3	296	5	Q22389	Q22389 caenorhabdi
37	8	3.3	302	5	Q19725	Q19725 caenorhabdi
38	8	3.3	305	4	Q9UDF6	Q9udf6 homo sapien
39	8	3.3	307	11	Q63742	Q63742 rattus sp.
40	8	3.3	307	11	Q62239	Q62239 mus musculu
41	8	3.3	316	4	Q9BV39	Q9bv39 homo sapien
42	8	3.3	322	4	Q9UHS4	Q9uhs4 homo sapien
43	8	3.3	333	5	Q19050	Q19050 caenorhabdi
44	8	3.3	337	11	Q8C972	Q8c972 mus musculu
45	8	3.3	349	4	Q99018	Q99018 homo sapien

ALIGNMENTS

RESULT 1
Q96CG8
ID Q96CG8 PRELIMINARY; PRT; 243 AA.
AC Q96CG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 1110014B07 gene (Collagen triple helix
DE repeat-containing protein 1).
GN CTHRC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic smooth muscle;
RA Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RT "Expression of the novel collagen triple helix repeat-containing gene
RT (Cthrc1) suggests functions in multiple organ systems.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014245; AAH14245.1; -.
DR EMBL; AY136825; AAN15749.1; -.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF01391; Collagen; 1.
SQ SEQUENCE 243 AA; 26224 MW; A11FFEB1C66867F9 CRC64;

Query Match 70.0%; Score 170; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133

```
Qy        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193

Qy        194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243


RESULT 2
Q8IX63
ID   Q8IX63      PRELIMINARY;      PRT;   232 AA.
AC   Q8IX63;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   NTMC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sanuki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
RT   "Novel polypeptide found in human cornea cDNA library.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF395488; AAO17919.1; -.
SQ   SEQUENCE   232 AA;  25163 MW;  E9D4BC30304837ED CRC64;

  Query Match             69.5%;  Score 169;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-166;
  Matches  169;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 119

Qy        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 179

Qy        194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELP 242
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELP 228


RESULT 3
Q9D1D6
ID   Q9D1D6      PRELIMINARY;      PRT;   245 AA.
AC   Q9D1D6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   1110014B07Rik protein.
GN   CTHRC1 OR 1110014B07RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003674; BAB22930.1; -.
DR   MGD; MGI:1915838; Cthrc1.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 1.
SQ   SEQUENCE   245 AA;  26460 MW;  14951B87D8181A0E CRC64;

  Query Match             45.7%;  Score 111;  DB 11;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-106;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 135

Qy        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPE 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPE 186


RESULT 4
Q8CG08
ID   Q8CG08      PRELIMINARY;      PRT;   245 AA.
AC   Q8CG08;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Collagen triple helix repeat-containing protein 1.
GN   CTHRC1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Lehnert W., Moore D.P., Harmon K.J., Mancini M.L., Lindner V.;
RT   "Expression of the novel collagen triple helix repeat-containing gene
RT   (Cthrc1) suggests functions in multiple organ systems.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY136824; AAN15748.1; -.
SQ   SEQUENCE   245 AA;  26424 MW;  2296FD6DCDBA21F2 CRC64;

  Query Match             45.7%;  Score 111;  DB 11;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-106;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 135

Qy        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPE 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPE 186


RESULT 5
Q9UMM7
ID   Q9UMM7      PRELIMINARY;      PRT;    41 AA.
AC   Q9UMM7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
```

```
DE   Alpha-1 type I collagen (Fragment).
GN   COL1A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83064528; PubMed=6183642;
RA   Chu M.L., Myers J.C., Bernard M.P., Ding J.F., Ramirez F.;
RT   "Cloning and characterization of five overlapping cDNAs specific for
RT   the human pro alpha 1(I) collagen chain.";
RL   Nucleic Acids Res. 10:5925-5934(1982).
DR   EMBL; J00111; AAA52290.1; -.
DR   InterPro; IPR000087; Collagen.
DR   Pfam; PF01391; Collagen; 1.
KW   Collagen.
FT   NON_TER       1      1
FT   NON_TER      41     41
SQ   SEQUENCE   41 AA;  3771 MW;  1B9D591B06A6C800 CRC64;

  Query Match             3.7%;  Score 9;  DB 4;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db         26 PGRDGSPGA 34


RESULT 6
P90741
ID   P90741      PRELIMINARY;      PRT;   144 AA.
AC   P90741;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   C02F4.3 protein.
GN   C02F4.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cummings P.N.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z81032; CAB02722.1; -.
DR   WormPep; C02F4.3; CE07854.
SQ   SEQUENCE   144 AA;  16112 MW;  907F9DDB1ACC1762 CRC64;

  Query Match             3.7%;  Score 9;  DB 5;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 0.67;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         67 LLLLLLLQL 75


RESULT 7
Q9AVM0
ID   Q9AVM0      PRELIMINARY;      PRT;   501 AA.
AC   Q9AVM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Cytochrome P450.
GN   ASPI-2.
OS   Asparagus officinalis (Garden asparagus).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC   Asparagus.
OX   NCBI_TaxID=4686;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Shoot;
RA   Imaishi H., Iwai C., Ohkawa H.;
RT   "Molecular cloning of Cytochrome P450 cDNA involved in the Seedling of
RT   Asparagus.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR   EMBL; AB037245; BAB40324.1; -.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   501 AA;  56336 MW;  8593A426B5C21D5A CRC64;

  Query Match             3.7%;  Score 9;  DB 10;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 2.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         13 LLLLLLLQL 21


RESULT 8
Q9ASN8
ID   Q9ASN8      PRELIMINARY;      PRT;   558 AA.
AC   Q9ASN8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P0554D10.9 protein.
GN   P0554D10.9.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT   clone:P0554D10.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP002869; BAB39225.1; -.
DR   Gramene; Q9ASN8; -.
DR   InterPro; IPR002123; Acyltransferase.
DR   SMART; SM00563; PlsC; 1.
SQ   SEQUENCE   558 AA;  60411 MW;  7893EDF390B716B9 CRC64;

  Query Match             3.7%;  Score 9;  DB 10;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 LRGLLLLLL 21
              |||||||||
Db         93 LRGLLLLLL 101


RESULT 9
Q921B6
ID   Q921B6      PRELIMINARY;      PRT;   870 AA.
AC   Q921B6;
```

```
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ApoE receptor-2.
GN   LRP8 OR APOER2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21303597; PubMed=11294845;
RA   Brandes C., Kahr L., Stockinger W., Hiesberger T., Schneider W.J.,
RA   Nimpf J.;
RT   "Alternative splicing in the ligand binding domain of mouse ApoE
RT   receptor-2 produces receptor variants binding reelin but not alpha2-
RT   macroglobulin.";
RL   J. Biol. Chem. 276:22160-22169(2001).
DR   EMBL; AJ312058; CAC38356.1; -.
DR   MGD; MGI:1340044; Lrp8.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00057; ldl_recept_a; 5.
DR   Pfam; PF00058; ldl_recept_b; 5.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00192; LDLa; 5.
DR   SMART; SM00135; LY; 5.
DR   PROSITE; PS00010; ASX_HYDROXYL; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS01209; LDLRA_1; 5.
DR   PROSITE; PS50068; LDLRA_2; 5.
KW   EGF-like domain; Receptor.
SQ   SEQUENCE   870 AA;  96268 MW;  FCD3982FDE18E3E0 CRC64;

  Query Match             3.7%;  Score 9;  DB 11;  Length 870;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         14 LLLLLLLQL 22


RESULT 10
Q924X6
ID   Q924X6      PRELIMINARY;      PRT;   996 AA.
AC   Q924X6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Apolipoprotein E receptor 2 precursor.
GN   LRP8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98352008; PubMed=9685741;
RA   Kim H.-J., Kim D.-H., Magoori K., Saeki S., Yamamoto T.;
RT   "Evolution of the Apolipoprotein E Receptor 2 Gene by Exon Loss.";
RL   J. Biochem. 124:451-456(1998).
DR   EMBL; D85463; BAB46965.1; -.
DR   MGD; MGI:1340044; Lrp8.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   Pfam; PF00057; ldl_recept_a; 8.
DR   Pfam; PF00058; ldl_recept_b; 5.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00192; LDLa; 8.
DR   SMART; SM00135; LY; 5.
DR   PROSITE; PS00010; ASX_HYDROXYL; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01187; EGF_CA; 1.
DR   PROSITE; PS01209; LDLRA_1; 8.
DR   PROSITE; PS50068; LDLRA_2; 8.
KW   EGF-like domain; Lipoprotein; Receptor; Signal.
FT   SIGNAL        1     35       POTENTIAL.
FT   CHAIN        36    996       APOLIPOPROTEIN E RECEPTOR 2.
SQ   SEQUENCE   996 AA;  109833 MW;  51DD430ACE572529 CRC64;

  Query Match             3.7%;  Score 9;  DB 11;  Length 996;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         14 LLLLLLLQL 22


RESULT 11
O76045
ID   O76045      PRELIMINARY;      PRT;  1461 AA.
AC   O76045;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Pro alpha 1(I) collagen.
GN   COL1A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85130970; PubMed=2857713;
RA   Chu M.L., de Wet W., Bernard M., Ramirez F.;
RT   "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
RT   Promoter structure, AluI repeats, and polymorphic transcripts.";
RL   J. Biol. Chem. 260:2315-2320(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88329734; PubMed=2843432;
RA   D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.;
RT   "Complete nucleotide sequence of the region encompassing the first
RT   twenty-five exons of the human pro alpha 1(I) collagen gene.";
RL   Gene 67:105-115(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89025644; PubMed=3178743;
RA   Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
RA   Jaenisch R., Prockop D.J.;
RT   "Structure of a full-length cDNA clone for the prepro alpha 1(I) chain
RT   of human type I procollagen.";
RL   Biochem. J. 253:919-922(1988).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91138770; PubMed=1995349;
RA   Maatta A., Bornstein P., Penttinen R.P.;
RT   "Highly conserved sequences in the 3'-untranslated region of the
RT   COL1A1 gene bind cell-specific nuclear proteins.";
RL   FEBS Lett. 279:9-13(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92157916; PubMed=1787829;
```

```
RA   Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning C.,
RA   Olsen A.S., Prockop D.J.;
RT   "Completion of the last half of the structure of the human gene for
RT   the Pro alpha 1 (I) chain of type I procollagen (COL1A1).";
RL   Matrix 11:375-379(1991).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98107942; PubMed=9443882;
RA   Korkko J., Ala-Kokko L., De Paepe A., Nuytinck L., Earley J.,
RA   Prockop D.J.;
RT   "Analysis of the COL1A1 and COL1A2 genes by PCR amplification and
RT   scanning by conformation-sensitive gel electrophoresis identifies only
RT   COL1A1 mutations in 15 patients with osteogenesis imperfecta type I:
RT   identification of common sequences of null-allele mutations.";
RL   Am. J. Hum. Genet. 62:98-110(1998).
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Korkko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
RA   Ala-Kokko L.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF017178; AAB94054.2; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF01410; COLFI; 1.
DR   Pfam; PF01391; Collagen; 18.
DR   Pfam; PF00093; vwc; 1.
DR   ProDom; PD000007; Collagen; 2.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01208; VWFC; 1.
KW   Collagen.
SQ   SEQUENCE   1461 AA;  138630 MW;  9ACF6DE30EA78E21 CRC64;

  Query Match             3.7%;  Score 9;  DB 4;  Length 1461;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1021 PGRDGSPGA 1029


RESULT 12
Q8N473
ID   Q8N473      PRELIMINARY;      PRT;  1464 AA.
AC   Q8N473;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC036531; AAH36531.1; -.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR000885; Fib_collagen_C.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF01410; COLFI; 1.
DR   Pfam; PF01391; Collagen; 18.
DR   ProDom; PD000007; Collagen; 2.
DR   ProDom; PD002078; Fib_collagen_C; 1.
DR   SMART; SM00038; COLFI; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01208; VWFC; 1.
KW   Hypothetical protein; Collagen.
SQ   SEQUENCE   1464 AA;  139011 MW;  B0581F8D1C89DDE8 CRC64;

  Query Match             3.7%;  Score 9;  DB 4;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1024 PGRDGSPGA 1032


RESULT 13
Q8K3I2
ID   Q8K3I2      PRELIMINARY;      PRT;    59 AA.
AC   Q8K3I2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Novel secreted protein precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD-1;
RA   Moffatt P., Salois P., Lanctot C., Gaumond M.-H., St-Amant N.,
RA   Godin E.;
RT   "Engineered viruses to select genes encoding secreted and membrane-
RT   bound proteins in mammalian cells.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY100450; AAM47508.1; -.
KW   Signal.
FT   SIGNAL       1     31       POTENTIAL.
FT   NON_TER     59     59
SQ   SEQUENCE   59 AA;  6775 MW;  E88594100AF0C8B0 CRC64;

  Query Match             3.3%;  Score 8;  DB 11;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GLLLLLL 22
              |||||||
Db         14 GLLLLLL 21


RESULT 14
Q91ZH3
ID   Q91ZH3      PRELIMINARY;      PRT;    65 AA.
AC   Q91ZH3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Endothelial and smooth muscle cell-derived neuropilin-like protein
DE   (Fragment).
GN   ESDN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RX   PubMed=11447234;
RA   Kobuke K., Furukawa Y., Sugai M., Tanigaki K., Ohashi N.,
RA   Matsumori A., Sasayama S., Honjo T., Tashiro K.;
RT   "ESDN, a Novel Neuropilin-like Membrane Protein Cloned from Vascular
RT   Cells with the Longest Secretory Signal Sequence among Eukaryotes, Is
RT   Up-regulated after Vascular Injury.";
RL   J. Biol. Chem. 276:34105-34114(2001).
DR   EMBL; AF442820; AAL30434.1; -.
FT   NON_TER      65     65
SQ   SEQUENCE   65 AA;  6452 MW;  278864A1DE2E8D50 CRC64;
```

```
  Query Match             3.3%;  Score 8;  DB 11;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQ 23
              ||||||||
Db         52 LLLLLLLQ 59


RESULT 15
Q9D9P8
ID   Q9D9P8      PRELIMINARY;      PRT;   108 AA.
AC   Q9D9P8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1700034O15Rik protein.
GN   1700034O15RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK006606; BAB24671.1; -.
DR   MGD; MGI:1923856; 1700034O15Rik.
SQ   SEQUENCE   108 AA;  12138 MW;  154E27F37C5B6101 CRC64;

  Query Match             3.3%;  Score 8;  DB 11;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQ 23
              ||||||||
Db         17 LLLLLLLQ 24


Search completed: August 13, 2003, 13:40:22
Job time : 97 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:36:43 ; Search time 30 Seconds
(without alignments)
342.718 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	70.0	276	4	US-09-205-258-958	Sequence 958, App
2	88	36.2	243	4	US-09-489-847-205	Sequence 205, App
3	66	27.2	66	4	US-09-205-258-962	Sequence 962, App
4	52	21.4	52	4	US-09-205-258-961	Sequence 961, App
5	51	21.0	51	4	US-09-205-258-963	Sequence 963, App
6	40	16.5	93	4	US-09-489-847-240	Sequence 240, App
7	40	16.5	93	4	US-09-489-847-362	Sequence 362, App
8	30	12.3	52	4	US-09-205-258-960	Sequence 960, App
9	9	3.7	654	4	US-09-252-991A-25801	Sequence 25801, A
10	9	3.7	905	4	US-09-369-364A-9	Sequence 9, Appli
11	9	3.7	1057	3	US-08-931-820-1	Sequence 1, Appli
12	9	3.7	1341	3	US-08-963-825-18	Sequence 18, Appl
13	9	3.7	1341	4	US-09-500-811-18	Sequence 18, Appl
14	9	3.7	1341	4	US-09-570-573-18	Sequence 18, Appl
15	9	3.7	1341	4	US-09-548-608-18	Sequence 18, Appl
16	9	3.7	1461	4	US-09-585-887-9	Sequence 9, Appli
17	9	3.7	1461	4	US-09-289-578-9	Sequence 9, Appli
18	8	3.3	20	3	US-08-918-288-51	Sequence 51, Appl
19	8	3.3	20	3	US-08-918-288-56	Sequence 56, Appl
20	8	3.3	20	3	US-09-282-357-51	Sequence 51, Appl
21	8	3.3	20	3	US-09-282-357-56	Sequence 56, Appl
22	8	3.3	20	4	US-09-059-625-38	Sequence 38, Appl
23	8	3.3	71	4	US-09-059-625-7	Sequence 7, Appli
24	8	3.3	72	4	US-09-059-625-4	Sequence 4, Appli
25	8	3.3	143	4	US-09-227-357-192	Sequence 192, App
26	8	3.3	151	4	US-09-059-625-32	Sequence 32, Appl
27	8	3.3	151	4	US-09-059-625-43	Sequence 43, Appl
28	8	3.3	151	4	US-09-059-625-46	Sequence 46, Appl
29	8	3.3	151	4	US-09-059-625-59	Sequence 59, Appl
30	8	3.3	155	4	US-09-059-625-62	Sequence 62, Appl
31	8	3.3	158	4	US-09-059-625-1	Sequence 1, Appli
32	8	3.3	159	4	US-09-059-625-64	Sequence 64, Appl
33	8	3.3	165	2	US-08-709-924-2	Sequence 2, Appli
34	8	3.3	165	2	US-08-709-925-2	Sequence 2, Appli
35	8	3.3	165	4	US-08-709-948-2	Sequence 2, Appli
36	8	3.3	165	4	US-09-220-415-2	Sequence 2, Appli
37	8	3.3	181	3	US-08-918-288-36	Sequence 36, Appl
38	8	3.3	181	3	US-09-282-357-36	Sequence 36, Appl
39	8	3.3	181	4	US-09-059-625-66	Sequence 66, Appl
40	8	3.3	184	4	US-09-059-625-67	Sequence 67, Appl
41	8	3.3	186	4	US-09-059-625-68	Sequence 68, Appl
42	8	3.3	203	4	US-09-059-625-85	Sequence 85, Appl
43	8	3.3	203	4	US-09-059-625-88	Sequence 88, Appl
44	8	3.3	204	4	US-09-059-625-35	Sequence 35, Appl
45	8	3.3	204	4	US-09-059-625-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-205-258-958
; Sequence 958, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

```
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 958
;   LENGTH: 276
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (10)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-958

  Query Match             70.0%;  Score 170;  DB 4;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-157;
  Matches  170;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 166

Qy        134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 226

Qy        194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 276


RESULT 2
US-09-489-847-205
; Sequence 205, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-205

  Query Match             36.2%;  Score 88;  DB 4;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 2e-77;
  Matches   88;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 RWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWV 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 RWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWV 215

Qy        216 GTCSDYPKGDASTGWNSVSRIIIEELPK 243
              ||||||||||||||||||||||||||||
Db        216 GTCSDYPKGDASTGWNSVSRIIIEELPK 243


RESULT 3
US-09-205-258-962
; Sequence 962, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
```

```
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 962
;   LENGTH: 66
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-205-258-962

  Query Match             27.2%;  Score 66;  DB 4;  Length 66;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-56;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        128 FTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNS 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNS 60

Qy        188 TINIHR 193
                  ||||||
Db         61 TINIHR 66


RESULT 4
US-09-205-258-961
; Sequence 961, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
```

```
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 961
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-205-258-961

  Query Match             21.4%;  Score 52;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-43;
  Matches   52;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         77 TPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTF 52


RESULT 5
US-09-205-258-963
; Sequence 963, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 963
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-205-258-963

  Query Match             21.0%;  Score 51;  DB 4;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-42;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        193 RTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 51


RESULT 6
```

```
US-09-489-847-240
; Sequence 240, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-240

  Query Match           16.5%;  Score 40;  DB 4;  Length 93;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-31;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40
              ||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40


RESULT 7
US-09-489-847-362
; Sequence 362, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 362
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-362

  Query Match           16.5%;  Score 40;  DB 4;  Length 93;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-31;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40
              ||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40


RESULT 8
US-09-205-258-960
; Sequence 960, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: 207 Human Secreted Proteins
;  FILE REFERENCE: PZ007P1
;  CURRENT APPLICATION NUMBER: US/09/205,258
;  CURRENT FILING DATE: 1998-12-04
;  EARLIER APPLICATION NUMBER: PCT/US98/11422
;  EARLIER FILING DATE: 1998-06-04
;  EARLIER APPLICATION NUMBER: 60/048,885
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,375
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,881
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,880
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,896
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,020
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,876
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,895
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,884
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,894
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,971
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,882
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,899
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,893
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,900
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,901
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,892
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,915
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,019
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,970
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,972
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,916
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,373
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,875
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/049,374
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,917
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,949
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,974
              ||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKA 40
```

```
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,883
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,897
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,898
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,962
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,963
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,877
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/048,878
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/070,923
;  EARLIER FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 1227
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 960
;   LENGTH:.52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-205-258-960

  Query Match             12.3%;  Score 30;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-22;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         43 RQREVVDLYNGMCLQGPAGVPGRDGSPGAN 72
              ||||||||||||||||||||||||||||||
Db         15 RQREVVDLYNGMCLQGPAGVPGRDGSPGAN 44


RESULT 9
US-09-252-991A-25801
; Sequence 25801, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 25801
;   LENGTH: 654
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25801

  Query Match             3.7%;  Score 9;  DB 4;  Length 654;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RPQGPAASP 10
              |||||||||
Db        453 RPQGPAASP 461


RESULT 10
US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
;  APPLICANT:  Apte, Suneel
;  APPLICANT:  Hurskainen, Tiina L.
;  APPLICANT:  Hirohata, Satoshi
;  TITLE OF INVENTION:  Nucleic Acids Encoding Zinc Metalloproteases
;  FILE REFERENCE:  26473/4007/10-30-00
;  CURRENT APPLICATION NUMBER: US/09/369,364A
;  CURRENT FILING DATE:  1999-08-06
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 905
;   TYPE: PRT
;   ORGANISM: Mus musculus ADAMTS-8
US-09-369-364A-9

  Query Match             3.7%;  Score 9;  DB 4;  Length 905;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLLQLP 25
              |||||||||
Db         13 LLLLLLQLP 21


RESULT 11
US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Assay for collagen degradation
;    NUMBER OF SEQUENCES:  4
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/931,820
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 96202596.1
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1057 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Collagen type I
US-08-931-820-1

  Query Match             3.7%;  Score 9;  DB 3;  Length 1057;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        863 PGRDGSPGA 871


RESULT 12
US-08-963-825-18
; Sequence 18, Application US/08963825
; Patent No. 6110689
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Qvist, Per
;    APPLICANT:  Bonde, Martin
;    TITLE OF INVENTION:  A Method for Assaying Collagen Fragments
;    TITLE OF INVENTION:  in Body Fluids, A Test Kit and Means for Carrying Out the
;    TITLE OF INVENTION:  Method and Use of the Method to Diagnose the Presence of
;    TITLE OF INVENTION:  Disorders Associated with the Metabolism of
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/963,825
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/187,319
;      FILING DATE:  21-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gogoris, Adda C
;      REGISTRATION NUMBER:  29,714
;      REFERENCE/DOCKET NUMBER:  4305/08701
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1341 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  COLLAGEN ALPHA 1 (I)
US-08-963-825-18

  Query Match             3.7%;  Score 9;  DB 3;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        900 PGRDGSPGA 908


RESULT 13
US-09-500-811-18
; Sequence 18, Application US/09500811
; Patent No. 6323314
;  GENERAL INFORMATION:
;    APPLICANT:  Qvist, Per
;    APPLICANT:  Bonde, Martin
;    TITLE OF INVENTION:  A Method for Assaying Collagen Fragments
;    TITLE OF INVENTION:  in Body Fluids, A Test Kit and Means for Carrying Out the
;    TITLE OF INVENTION:  Method and Use of the Method to Diagnose the Presence of
;    TITLE OF INVENTION:  Disorders Associated with the Metabolism of
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/500,811
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,319
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gogoris, Adda C
;      REGISTRATION NUMBER:  29,714
;      REFERENCE/DOCKET NUMBER:  4305/08701
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1341 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  COLLAGEN ALPHA 1 (I)
US-09-500-811-18

  Query Match             3.7%;  Score 9;  DB 4;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        900 PGRDGSPGA 908


RESULT 14
US-09-570-573-18
; Sequence 18, Application US/09570573
; Patent No. 6342361
;  GENERAL INFORMATION:
;    APPLICANT:  Qvist, Per
;    APPLICANT:  Bonde, Martin
;    TITLE OF INVENTION:  A Method for Assaying Collagen Fragments
;    TITLE OF INVENTION:  in Body Fluids, A Test Kit and Means for Carrying Out the
;    TITLE OF INVENTION:  Method and Use of the Method to Diagnose the Presence of
;    TITLE OF INVENTION:  Disorders Associated with the Metabolism of
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/570,573
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,319
;      FILING DATE:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gogoris, Adda C
;      REGISTRATION NUMBER:  29,714
;      REFERENCE/DOCKET NUMBER:  4305/08701
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1341 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  COLLAGEN ALPHA 1 (I)
US-09-570-573-18

  Query Match             3.7%;  Score 9;  DB 4;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        900 PGRDGSPGA 908


RESULT 15
US-09-548-608-18
; Sequence 18, Application US/09548608
; Patent No. 6355442
;  GENERAL INFORMATION:
;    APPLICANT:  Qvist, Per
;    APPLICANT:  Bonde, Martin
;    TITLE OF INVENTION:  A Method for Assaying Collagen Fragments
;    TITLE OF INVENTION:  in Body Fluids, A Test Kit and Means for Carrying Out the
;    TITLE OF INVENTION:  Method and Use of the Method to Diagnose the Presence of
;    TITLE OF INVENTION:  Disorders Associated with the Metabolism of
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby PC
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/548,608
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/187,319
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gogoris, Adda C
;      REGISTRATION NUMBER:  29,714
;      REFERENCE/DOCKET NUMBER:  4305/08701
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-527-7700
;      TELEFAX:  212-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1341 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  COLLAGEN ALPHA 1 (I)
US-09-548-608-18

  Query Match             3.7%;  Score 9;  DB 4;  Length 1341;
  Best Local Similarity   100.0%;  Pred. No. 3.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        900 PGRDGSPGA 908


Search completed: August 13, 2003, 13:41:44
Job time : 30 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:40:28 ; Search time 56 Seconds
(without alignments)
568.461 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 492763 seqs, 131003257 residues

Word size : 6

Total number of hits satisfying chosen parameters: 16488

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	243	100.0	243	10	US-09-938-418-7	Sequence 7, Appli
2	243	100.0	243	11	US-09-946-374-352	Sequence 352, App
3	243	100.0	243	11	US-09-946-374-431	Sequence 431, App
4	243	100.0	243	12	US-10-015-387A-352	Sequence 352, App
5	243	100.0	243	12	US-10-015-387A-431	Sequence 431, App
6	243	100.0	243	12	US-10-063-735-122	Sequence 122, App
7	243	100.0	243	12	US-10-006-130A-352	Sequence 352, App
8	243	100.0	243	12	US-10-006-130A-431	Sequence 431, App
9	243	100.0	243	12	US-10-199-672-366	Sequence 366, App
10	243	100.0	243	14	US-10-006-867-122	Sequence 122, App
11	243	100.0	243	14	US-10-052-586-366	Sequence 366, App
12	243	100.0	243	14	US-10-007-805-514	Sequence 514, App
13	243	100.0	243	14	US-10-063-547-122	Sequence 122, App
14	243	100.0	243	15	US-10-174-590-366	Sequence 366, App
15	243	100.0	243	15	US-10-176-758-366	Sequence 366, App
16	243	100.0	243	15	US-10-175-737-366	Sequence 366, App
17	243	100.0	243	15	US-10-063-616-122	Sequence 122, App
18	243	100.0	243	15	US-10-173-706-366	Sequence 366, App
19	243	100.0	243	15	US-10-175-738-366	Sequence 366, App
20	243	100.0	243	15	US-10-175-752-366	Sequence 366, App
21	243	100.0	243	15	US-10-176-482-366	Sequence 366, App
22	243	100.0	243	15	US-10-176-757-366	Sequence 366, App
23	243	100.0	243	15	US-10-176-913-366	Sequence 366, App
24	243	100.0	243	15	US-10-180-552-366	Sequence 366, App
25	243	100.0	243	15	US-10-180-557-366	Sequence 366, App
26	243	100.0	243	15	US-10-076-622-514	Sequence 514, App
27	243	100.0	243	15	US-10-063-502-122	Sequence 122, App
28	243	100.0	243	15	US-10-173-700-366	Sequence 366, App
29	243	100.0	243	15	US-10-174-572-366	Sequence 366, App
30	243	100.0	243	15	US-10-174-579-366	Sequence 366, App
31	243	100.0	243	15	US-10-174-582-366	Sequence 366, App
32	243	100.0	243	15	US-10-174-588-366	Sequence 366, App
33	243	100.0	243	15	US-10-175-739-366	Sequence 366, App
34	243	100.0	243	15	US-10-175-740-366	Sequence 366, App
35	243	100.0	243	15	US-10-175-743-366	Sequence 366, App
36	243	100.0	243	15	US-10-176-488-366	Sequence 366, App
37	243	100.0	243	15	US-10-176-492-366	Sequence 366, App
38	243	100.0	243	15	US-10-176-747-366	Sequence 366, App
39	243	100.0	243	15	US-10-176-750-366	Sequence 366, App
40	243	100.0	243	15	US-10-176-985-366	Sequence 366, App
41	243	100.0	243	15	US-10-176-987-366	Sequence 366, App
42	243	100.0	243	15	US-10-176-992-366	Sequence 366, App
43	243	100.0	243	15	US-10-176-993-366	Sequence 366, App
44	243	100.0	243	15	US-10-184-658-366	Sequence 366, App
45	243	100.0	243	15	US-10-176-991-366	Sequence 366, App

ALIGNMENTS

RESULT 1
US-09-938-418-7
; Sequence 7, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Gurney,Austin L.
; APPLICANT: Polakis,Paul
; APPLICANT: Williams,P.Mickey
; APPLICANT: Wood,William I.
; APPLICANT: Wu,Thomas D.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342

```
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-938-418-7

  Query Match             100.0%;  Score 243;  DB 10;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 2
US-09-946-374-352
; Sequence 352, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
```

; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 243; DB 11; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.7e-214;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 3
US-09-946-374-431
; Sequence 431, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01

```
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match            100.0%;  Score 243;  DB 11;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 4
US-10-015-387A-352
; Sequence 352, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C54
;  CURRENT APPLICATION NUMBER: US/10/015,387A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-015-387A-352

  Query Match            100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 5
US-10-015-387A-431
; Sequence 431, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
```

```
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C54
;  CURRENT APPLICATION NUMBER: US/10/015,387A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-015-387A-431
```

```
  Query Match            100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 6
US-10-063-735-122
; Sequence 122, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,735
;  CURRENT FILING DATE:  2002-05-08
;       Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-735-122
```

```
  Query Match            100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 7
US-10-006-130A-352
; Sequence 352, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-130A-352
```

```
  Query Match            100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
```

```
                ||||
Db        241 LPK 243


RESULT 8
US-10-006-130A-431
; Sequence 431, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-130A-431

  Query Match             100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
                |||
Db        241 LPK 243


RESULT 9
US-10-199-672-366
; Sequence 366, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/199,672
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-199-672-366

  Query Match             100.0%;  Score 243;  DB 12;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
                |||
Db        241 LPK 243


RESULT 10
US-10-006-867-122
; Sequence 122, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/096012
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096757
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/096949
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/096959
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/097954
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097971
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/097979
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23

```
;  PRIOR APPLICATION NUMBER: 60/114223
;  PRIOR FILING DATE: 1998-12-30
;  PRIOR APPLICATION NUMBER: 60/115614
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116527
;  PRIOR FILING DATE: 1999-01-20
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/119285
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: 60/119287
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: 60/119525
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/119549
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: 60/120014
;  PRIOR FILING DATE: 1999-02-11
;  PRIOR APPLICATION NUMBER: 60/129122
;  PRIOR FILING DATE: 1999-04-13
;  PRIOR APPLICATION NUMBER: 60/129674
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/131291
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/138387
;  PRIOR FILING DATE: 1999-06-09
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/169495
;  PRIOR FILING DATE: 1999-12-07
;  PRIOR APPLICATION NUMBER: 60/175481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 60/191007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/199397
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/380139
;  PRIOR FILING DATE: 1998-08-25
;  PRIOR APPLICATION NUMBER: 09/311832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 09/380137
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/380138
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/380142

  Query Match           100.0%;  Score 243;  DB 14;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 11
US-10-052-586-366

; Sequence 366, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/052,586
;  CURRENT FILING DATE:  2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063564
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063734
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063870
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066120
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/066466
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069425
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: 60/069870
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/068017
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
```

; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 243; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.7e-214;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 12
US-10-007-805-514
; Sequence 514, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C10
;  CURRENT APPLICATION NUMBER: US/10/007,805
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 593
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-805-514

  Query Match            100.0%;  Score 243;  DB 14;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 13
US-10-063-547-122
; Sequence 122, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,547
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 122
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-547-122

  Query Match            100.0%;  Score 243;  DB 14;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
US-10-174-590-366
; Sequence 366, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-174-590-366

  Query Match            100.0%;  Score 243;  DB 15;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
US-10-176-758-366
; Sequence 366, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 366
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-758-366

  Query Match            100.0%;  Score 243;  DB 15;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-214;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

Search completed: August 13, 2003, 13:49:38
Job time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:38:13 ; Search time 374 Seconds
(without alignments)
565.500 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 5580241 seqs, 870357830 residues

Word size : 6

Total number of hits satisfying chosen parameters: 47375

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	243	100.0	243	1	PCT-US02-02781-4559	Sequence 4559, Ap
2	243	100.0	243	1	PCT-US02-12378-514	Sequence 514, App
3	243	100.0	243	23	US-09-834-759-514	Sequence 514, App
4	243	100.0	243	24	US-09-938-418-7	Sequence 7, Appli
5	243	100.0	243	24	US-09-946-374-352	Sequence 352, App
6	243	100.0	243	24	US-09-946-374-431	Sequence 431, App
7	243	100.0	243	26	US-10-006-041A-352	Sequence 352, App
8	243	100.0	243	26	US-10-006-041A-431	Sequence 431, App
9	243	100.0	243	26	US-10-006-063A-352	Sequence 352, App
10	243	100.0	243	26	US-10-006-063A-431	Sequence 431, App
11	243	100.0	243	26	US-10-006-116A-352	Sequence 352, App
12	243	100.0	243	26	US-10-006-116A-431	Sequence 431, App
13	243	100.0	243	26	US-10-006-117A-352	Sequence 352, App
14	243	100.0	243	26	US-10-006-117A-431	Sequence 431, App
15	243	100.0	243	26	US-10-006-130A-352	Sequence 352, App
16	243	100.0	243	26	US-10-006-130A-431	Sequence 431, App
17	243	100.0	243	26	US-10-006-172A-352	Sequence 352, App
18	243	100.0	243	26	US-10-006-172A-431	Sequence 431, App
19	243	100.0	243	26	US-10-006-485A-352	Sequence 352, App
20	243	100.0	243	26	US-10-006-485A-431	Sequence 431, App
21	243	100.0	243	26	US-10-006-746A-352	Sequence 352, App
22	243	100.0	243	26	US-10-006-746A-431	Sequence 431, App
23	243	100.0	243	26	US-10-006-768A-352	Sequence 352, App
24	243	100.0	243	26	US-10-006-768A-431	Sequence 431, App
25	243	100.0	243	26	US-10-006-818A-352	Sequence 352, App
26	243	100.0	243	26	US-10-006-818A-431	Sequence 431, App
27	243	100.0	243	26	US-10-006-856A-352	Sequence 352, App
28	243	100.0	243	26	US-10-006-856A-431	Sequence 431, App
29	243	100.0	243	26	US-10-006-867-122	Sequence 122, App
30	243	100.0	243	26	US-10-007-194A-352	Sequence 352, App
31	243	100.0	243	26	US-10-007-194A-431	Sequence 431, App
32	243	100.0	243	26	US-10-007-236A-352	Sequence 352, App
33	243	100.0	243	26	US-10-007-236A-431	Sequence 431, App
34	243	100.0	243	26	US-10-007-805-514	Sequence 514, App
35	243	100.0	243	26	US-10-011-671A-352	Sequence 352, App
36	243	100.0	243	26	US-10-011-671A-431	Sequence 431, App
37	243	100.0	243	26	US-10-011-692A-352	Sequence 352, App
38	243	100.0	243	26	US-10-011-692A-431	Sequence 431, App
39	243	100.0	243	26	US-10-011-795A-352	Sequence 352, App
40	243	100.0	243	26	US-10-011-795A-431	Sequence 431, App
41	243	100.0	243	26	US-10-011-795B-352	Sequence 352, App
42	243	100.0	243	26	US-10-011-795B-431	Sequence 431, App
43	243	100.0	243	26	US-10-011-833A-352	Sequence 352, App
44	243	100.0	243	26	US-10-011-833A-431	Sequence 431, App
45	243	100.0	243	26	US-10-012-064A-352	Sequence 352, App

ALIGNMENTS

RESULT 1
PCT-US02-02781-4559
; Sequence 4559, Application PC/TUS0202781
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566PC
; CURRENT APPLICATION NUMBER: PCT/US02/02781
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4559
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-02781-4559

Query Match 100.0%; Score 243; DB 1; Length 243;

```
  Best Local Similarity   100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 2
PCT-US02-12378-514
; Sequence 514, Application PC/TUS0212378
; GENERAL INFORMATION:
;  APPLICANT: Houghton, Raymond L.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Durham, Margarita
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.47003PC
;  CURRENT APPLICATION NUMBER: PCT/US02/12378
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-12378-514

  Query Match             100.0%;  Score 243;  DB 1;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 3
US-09-834-759-514
; Sequence 514, Application US/09834759
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C9
;  CURRENT APPLICATION NUMBER: US/09/834,759
;  CURRENT FILING DATE:  2001-04-13
;  NUMBER OF SEQ ID NOS: 547
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 514
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-759-514

  Query Match             100.0%;  Score 243;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 4
US-09-938-418-7
; Sequence 7, Application US/09938418
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Polakis,Paul
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Wu,Thomas D.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF TUMOR
;  FILE REFERENCE: P5009R1
;  CURRENT APPLICATION NUMBER: US/09/938,418
```

```
;  CURRENT FILING DATE:  2001-08-23
;  PRIOR APPLICATION NUMBER: 60/081,071
;  PRIOR FILING DATE: 1998-04-07
;  PRIOR APPLICATION NUMBER: 60/085,697
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/097,022
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/101,922
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/103,679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: PCT/US99/05028
;  PRIOR FILING DATE: 1999-03-08
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: PCT/US99/20111
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US00/04342
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-938-418-7

  Query Match           100.0%;  Score 243;  DB 24;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

```
RESULT 5
US-09-946-374-352
; Sequence 352, Application US/09946374
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
```

; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 243; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.5e-210;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 6
US-09-946-374-431
; Sequence 431, Application US/09946374
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
```

```
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27

  Query Match           100.0%;  Score 243;  DB 24;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 7
US-10-006-041A-352
; Sequence 352, Application US/10006041A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C8
;  CURRENT APPLICATION NUMBER: US/10/006,041A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-041A-352

  Query Match           100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
```

```
Db        241 LPK 243


RESULT 8
US-10-006-041A-431
; Sequence 431, Application US/10006041A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C8
;  CURRENT APPLICATION NUMBER: US/10/006,041A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-041A-431

  Query Match           100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 9
US-10-006-063A-352
; Sequence 352, Application US/10006063A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C3
;  CURRENT APPLICATION NUMBER: US/10/006,063A
;  CURRENT FILING DATE:  2002-03-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-063A-352

  Query Match           100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 10
US-10-006-063A-431
; Sequence 431, Application US/10006063A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C3
;  CURRENT APPLICATION NUMBER: US/10/006,063A
;  CURRENT FILING DATE:  2002-03-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-063A-431
```

```
  Query Match           100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 11
US-10-006-116A-352
; Sequence 352, Application US/10006116A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
```

; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 243; DB 26; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.5e-210;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 12
US-10-006-116A-431
; Sequence 431, Application US/10006116A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21

```
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match            100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 13
US-10-006-117A-352
; Sequence 352, Application US/10006117A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-117A-352

  Query Match            100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
US-10-006-117A-431
; Sequence 431, Application US/10006117A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 431
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-006-117A-431

  Query Match            100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
US-10-006-130A-352
; Sequence 352, Application US/10006130A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 352
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-130A-352

  Query Match             100.0%;  Score 243;  DB 26;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-210;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


Search completed: August 13, 2003, 13:48:06
Job time : 375 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:38:43 ; Search time 21 Seconds
(without alignments)
252.569 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 243
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105250 seqs, 21826969 residues

Word size : 6

Total number of hits satisfying chosen parameters: 763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	70.0	243	1	PCT-US02-29560A-203	Sequence 203, App
2	9	3.7	80	6	US-10-603-113-23275	Sequence 23275, A
3	9	3.7	996	6	US-10-464-368-85	Sequence 85, Appl
4	9	3.7	1164	7	US-60-487-610-2411	Sequence 2411, Ap
5	9	3.7	1164	7	US-60-485-450-1525	Sequence 1525, Ap
6	9	3.7	1284	7	US-60-487-610-2407	Sequence 2407, Ap
7	9	3.7	1284	7	US-60-485-450-1521	Sequence 1521, Ap
8	9	3.7	1464	1	PCT-US02-18638A-36	Sequence 36, Appl
9	9	3.7	1464	6	US-10-291-265-243	Sequence 243, App
10	9	3.7	1464	7	US-60-487-610-2409	Sequence 2409, Ap
11	9	3.7	1464	7	US-60-485-450-1523	Sequence 1523, Ap
12	8	3.3	82	6	US-10-603-113-21887	Sequence 21887, A
13	8	3.3	178	7	US-60-487-610-2653	Sequence 2653, Ap
14	8	3.3	178	7	US-60-485-450-1694	Sequence 1694, Ap
15	8	3.3	181	4	US-08-867-587B-34	Sequence 34, Appl
16	8	3.3	234	4	US-08-867-587B-4	Sequence 4, Appli
17	8	3.3	234	4	US-08-867-587B-7	Sequence 7, Appli
18	8	3.3	234	4	US-08-867-587B-19	Sequence 19, Appl
19	8	3.3	234	4	US-08-867-587B-22	Sequence 22, Appl
20	8	3.3	237	4	US-08-867-587B-13	Sequence 13, Appl
21	8	3.3	237	4	US-08-867-587B-16	Sequence 16, Appl
22	8	3.3	254	6	US-10-408-765A-509	Sequence 509, App
23	8	3.3	265	4	US-08-867-587B-1	Sequence 1, Appli
24	8	3.3	265	4	US-08-867-587B-37	Sequence 37, Appl
25	8	3.3	366	6	US-10-408-765A-492	Sequence 492, App
26	8	3.3	486	7	US-60-487-836-10	Sequence 10, Appl
27	8	3.3	652	6	US-10-408-765A-1422	Sequence 1422, Ap
28	8	3.3	671	7	US-60-485-450-1335	Sequence 1335, Ap
29	8	3.3	828	7	US-60-487-610-2652	Sequence 2652, Ap
30	8	3.3	828	7	US-60-485-450-1693	Sequence 1693, Ap
31	8	3.3	893	6	US-10-369-072-38	Sequence 38, Appl
32	8	3.3	918	7	US-60-487-610-2650	Sequence 2650, Ap
33	8	3.3	918	7	US-60-485-450-1691	Sequence 1691, Ap
34	8	3.3	984	7	US-60-487-610-2168	Sequence 2168, Ap
35	8	3.3	984	7	US-60-485-450-1382	Sequence 1382, Ap
36	8	3.3	984	7	US-60-490-890-209	Sequence 209, App
37	8	3.3	987	7	US-60-487-610-2242	Sequence 2242, Ap
38	8	3.3	987	7	US-60-485-450-1437	Sequence 1437, Ap
39	8	3.3	1019	7	US-60-487-610-2651	Sequence 2651, Ap
40	8	3.3	1019	7	US-60-485-450-1692	Sequence 1692, Ap
41	8	3.3	1388	6	US-10-408-765A-1718	Sequence 1718, Ap
42	8	3.3	1416	7	US-60-490-890-773	Sequence 773, App
43	8	3.3	1472	7	US-60-490-890-769	Sequence 769, App
44	8	3.3	1475	7	US-60-490-890-771	Sequence 771, App
45	8	3.3	1531	7	US-60-490-890-767	Sequence 767, App

ALIGNMENTS

RESULT 1
PCT-US02-29560A-203
; Sequence 203, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-203

Query Match 70.0%; Score 170; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.4e-143;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          74 IPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRS 133

Qy         134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         134 NSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHR 193

Qy         194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         194 TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK 243
```

RESULT 2
US-10-603-113-23275
; Sequence 23275, Application US/10603113
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

```
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/10/603,113
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/248,796
;  PRIOR FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 23275
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-10-603-113-23275

  Query Match             3.7%;  Score 9;  DB 6;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 0.33;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db          1 LLLLLLLQL 9


RESULT 3
US-10-464-368-85
; Sequence 85, Application US/10464368
; GENERAL INFORMATION:
;  APPLICANT: Krumlauf, Robb
;  APPLICANT:  Ellies, Debra
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
;  FILE REFERENCE: 40716-IP-017
;  CURRENT APPLICATION NUMBER: US/10/464,368
;  CURRENT FILING DATE:  2003-06-16
;  PRIOR APPLICATION NUMBER: 60/388,970
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 996
;   TYPE: PRT
;   ORGANISM: MOUSE
US-10-464-368-85

  Query Match             3.7%;  Score 9;  DB 6;  Length 996;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LLLLLLLQL 24
              |||||||||
Db         14 LLLLLLLQL 22


RESULT 4
US-60-487-610-2411
; Sequence 2411, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2411
;   LENGTH: 1164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2411

  Query Match             3.7%;  Score 9;  DB 7;  Length 1164;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        724 PGRDGSPGA 732


RESULT 5
US-60-485-450-1525
; Sequence 1525, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1525
;   LENGTH: 1164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1525

  Query Match             3.7%;  Score 9;  DB 7;  Length 1164;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        724 PGRDGSPGA 732


RESULT 6
US-60-487-610-2407
; Sequence 2407, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2407
;   LENGTH: 1284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2407

  Query Match             3.7%;  Score 9;  DB 7;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        844 PGRDGSPGA 852


RESULT 7
US-60-485-450-1521
; Sequence 1521, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
```

```
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1521
;   LENGTH: 1284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1521

  Query Match             3.7%;  Score 9;  DB 7;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db        844 PGRDGSPGA 852


RESULT 8
PCT-US02-18638A-36
; Sequence 36, Application PC/TUS0218638A
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc. et al.
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035PC
;  CURRENT APPLICATION NUMBER: PCT/US02/18638A
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-18638A-36

  Query Match             3.7%;  Score 9;  DB 1;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1024 PGRDGSPGA 1032


RESULT 9
US-10-291-265-243
; Sequence 243, Application US/10291265
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang et al
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-017 (785)
;  CURRENT APPLICATION NUMBER: US/10/291,265
;  CURRENT FILING DATE:  2000-01-25
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-291-265-243

  Query Match             3.7%;  Score 9;  DB 6;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1024 PGRDGSPGA 1032


RESULT 10
US-60-487-610-2409
; Sequence 2409, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2409
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-487-610-2409

  Query Match             3.7%;  Score 9;  DB 7;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         63 PGRDGSPGA 71
              |||||||||
Db       1024 PGRDGSPGA 1032


RESULT 11
US-60-485-450-1523
; Sequence 1523, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1523
;   LENGTH: 1464
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-485-450-1523

  Query Match             3.7%;  Score 9;  DB 7;  Length 1464;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          63 PGRDGSPGA 71
               |||||||||
Db        1024 PGRDGSPGA 1032


RESULT 12
US-10-603-113-21887
; Sequence 21887, Application US/10603113
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/10/603,113
;  CURRENT FILING DATE:  2003-06-24
;  PRIOR APPLICATION NUMBER: US/09/248,796
;  PRIOR FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 21887
;    LENGTH: 82
;    TYPE: PRT
;    ORGANISM: Candida albicans
US-10-603-113-21887

  Query Match             3.3%;  Score 8;  DB 6;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 GLLLLLLL 22
               ||||||||
Db          31 GLLLLLLL 38


RESULT 13
US-60-487-610-2653
; Sequence 2653, Application US/60487610
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  HUANG, Hongjin
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
;  TITLE OF INVENTION:  METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001469
;  CURRENT APPLICATION NUMBER: US/60/487,610
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 97101
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2653
;    LENGTH: 178
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-60-487-610-2653

  Query Match             3.3%;  Score 8;  DB 7;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          85 GFKGEKGE 92
               ||||||||
Db          32 GFKGEKGE 39


RESULT 14
US-60-485-450-1694
; Sequence 1694, Application US/60485450
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/485,450
;  CURRENT FILING DATE:  2003-07-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1694
;    LENGTH: 178
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-60-485-450-1694

  Query Match             3.3%;  Score 8;  DB 7;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          85 GFKGEKGE 92
               ||||||||
Db          32 GFKGEKGE 39


RESULT 15
US-08-867-587B-34
; Sequence 34, Application US/08867587B
; GENERAL INFORMATION:
;  APPLICANT: Moyle, William R.
;  TITLE OF INVENTION: Methods for Altering Fertility
;  FILE REFERENCE: Moyl-001
;  CURRENT APPLICATION NUMBER: US/08/867,587B
;  CURRENT FILING DATE:  1997-06-02
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
;    LENGTH: 181
;    TYPE: PRT
;    ORGANISM: Rat leukemia virus
US-08-867-587B-34

  Query Match             3.3%;  Score 8;  DB 4;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 GLLLLLLL 22
               ||||||||
Db           6 GLLLLLLL 13


Search completed: August 13, 2003, 13:48:34
Job time : 21 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 11:07:09 ; Search time 4783 Seconds
(without alignments)
10751.286 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1257	100.0	1257	6	AX092390	AX092390 Sequence
2		1257	100.0	1257	6	AX376298	AX376298 Sequence
3		1257	100.0	1257	6	AX454660	AX454660 Sequence
4		1257	100.0	1257	6	AX459648	AX459648 Sequence
5		1257	100.0	1257	6	AX491138	AX491138 Sequence
6		1257	100.0	1257	6	AX697362	AX697362 Sequence
7		1231.6	98.0	1342	6	AR243851	AR243851 Sequence
8		1222.8	97.3	1286	6	AR243886	AR243886 Sequence
9		1217.2	96.8	1245	9	BC014245	BC014245 Homo sapi
10		1198.8	95.4	1221	9	AY136825	AY136825 Homo sapi
11		964.6	76.7	1215	9	AF395488	AF395488 Homo sapi
12	c	793	63.1	860	6	AX285214	AX285214 Sequence
13		728.8	58.0	732	6	BD006704	BD006704 Novel pol
14	c	682.2	54.3	683	6	AX375790	AX375790 Sequence
15	c	681.8	54.2	683	6	AR280558	AR280558 Sequence
16	c	681.8	54.2	683	6	AR283054	AR283054 Sequence
17	c	681.8	54.2	683	6	AX302743	AX302743 Sequence
18		664.2	52.8	1217	10	AY136824	AY136824 Rattus no
19		640.8	51.0	687	6	AX067343	AX067343 Sequence
20		539.8	42.9	160197	9	AP004221	AP004221 Homo sapi
21	c	539.8	42.9	176922	9	AC012213	AC012213 Homo sapi
22	c	532.2	42.3	560	6	AX339938	AX339938 Sequence
23	c	433.2	34.5	460	6	AX351434	AX351434 Sequence
24		431.2	34.3	471	6	AX340025	AX340025 Sequence
25		287	22.8	111496	9	AC069351	AC069351 Homo sapi
26		258	20.5	271	6	AX284686	AX284686 Sequence
27		232	18.5	346	6	AX198974	AX198974 Sequence
28		232	18.5	346	6	AX198975	AX198975 Sequence
29		231	18.4	231	6	AX209500	AX209500 Sequence
30		231	18.4	231	6	AX209501	AX209501 Sequence
31		228	18.1	525	6	AX198465	AX198465 Sequence
32		228	18.1	525	6	AX209011	AX209011 Sequence
33		219.6	17.5	74798	2	AC069352	AC069352 Homo sapi
34	c	196.6	15.6	270	6	AX332192	AX332192 Sequence
35	c	190.2	15.1	323534	2	AC121173	AC121173 Rattus no
36	c	186	14.8	235421	2	AC131363	AC131363 Rattus no
37	c	185.6	14.8	208553	2	AC145088	AC145088 Mus muscu
38	c	184.8	14.7	166810	9	AL590222	AL590222 Human DNA
39	c	132.8	10.6	475	6	AX284559	AX284559 Sequence
40		120.6	9.6	213269	5	AL844521	AL844521 Zebrafish
41		76.8	6.1	250029	3	AE014830	AE014830 Plasmodiu
42		75.2	6.0	335050	3	PFA929356	AL929356 Plasmodiu
43	c	71.8	5.7	246611	2	AC111404	AC111404 Rattus no
44		71.4	5.7	9483	6	AX251786	AX251786 Sequence
45		71.4	5.7	9483	6	AX345278	AX345278 Sequence

ALIGNMENTS

RESULT 1
AX092390
LOCUS AX092390 1257 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 121 from Patent WO0116318.
ACCESSION AX092390
VERSION AX092390.1 GI:13444509
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.

```
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0116318-A 121 08-MAR-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN

  Query Match           100.0%;  Score 1257;  DB 6;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-213;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 2
AX376298
LOCUS       AX376298               1257 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 365 from Patent WO0168848.
ACCESSION   AX376298
VERSION     AX376298.1  GI:19170540
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0168848-A 365 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN

  Query Match           100.0%;  Score 1257;  DB 6;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-213;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 3
AX454660

```
LOCUS       AX454660               1257 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 245 from Patent WO0208284.
ACCESSION   AX454660
VERSION     AX454660.1  GI:21713954
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 245 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN
```

Query Match 100.0%; Score 1257; DB 6; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.2e-213;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy          601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy          661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy          721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy          781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy          841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy          901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy          961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy         1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTT 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTT 1080

Qy         1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy         1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy         1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
RESULT 4
AX459648
LOCUS       AX459648                1257 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 2 from Patent WO0216602.
ACCESSION   AX459648
VERSION     AX459648.1  GI:21725519
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Polakis,P.,
            Williams,P.M., Wood,W.I., Wu,T.D. and Zhang,Z.
  TITLE     Compositions and methods for the diagnosis and treatment of tumor
  JOURNAL   Patent: WO 0216602-A 2 28-FEB-2002;
            GENENTECH, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN
```

```
  Query Match             100.0%;  Score 1257;  DB 6;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-213;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy           61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy          121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy          181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy          241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy          301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy          361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy          421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy          481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy          541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy          601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy          661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy          721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy          781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy          841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy          901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy          961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy         1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTT 1080
```

```
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 5
AX491138
LOCUS       AX491138               1257 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 245 from Patent WO0200690.
ACCESSION   AX491138
VERSION     AX491138.1  GI:22323906
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0200690-A 245 03-JAN-2002;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN

  Query Match           100.0%;  Score 1257;  DB 6;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-213;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 6
AX697362
LOCUS       AX697362               1257 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 430 from Patent WO0078961.
ACCESSION   AX697362
VERSION     AX697362.1  GI:29498494
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
```

```
          Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
          Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
          Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding
          the same
  JOURNAL Patent: WO 0078961-A 430 28-DEC-2000;
          Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      324 a    264 c    299 g    370 t
ORIGIN

  Query Match           100.0%;  Score 1257;  DB 6;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-213;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 7
AR243851
LOCUS       AR243851               1342 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 89 from patent US 6476195.
ACCESSION   AR243851
VERSION     AR243851.1  GI:27291344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1342)
  AUTHORS   Komatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A.,
            Shi,Y., LaFleur,D.W., Wei,Y.-F., Ni,J., Florence,K.A., Young,P.,
            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H. and
            Mucenski,M.
  TITLE     Secreted protein HNFGF20
  JOURNAL   Patent: US 6476195-A 89 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .1342
                     /organism="unknown"
BASE COUNT      405 a    268 c    300 g    369 t
ORIGIN

  Query Match           98.0%;  Score 1231.6;  DB 6;  Length 1342;
  Best Local Similarity  99.6%;  Pred. No. 4e-209;
  Matches 1245;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          8 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCC 67
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         12 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG-C 70

Qy         68 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 130

Qy        128 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 190

Qy        188 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 250
```

```
Qy        248 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 310

Qy        308 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTAC 367
              |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        311 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTAC 370

Qy        368 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 430

Qy        428 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 490

Qy        488 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 550

Qy        548 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 607
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        551 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTG 610

Qy        608 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 670

Qy        668 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 730

Qy        728 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 790

Qy        788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 850

Qy        848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 910

Qy        908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 970

Qy        968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1030

Qy       1028 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1090

Qy       1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1150

Qy       1148 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1151 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1210

Qy       1208 AAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1211 AAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAAAA 1260
```

```
RESULT 8
AR243886
LOCUS       AR243886               1286 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 124 from patent US 6476195.
ACCESSION   AR243886
VERSION     AR243886.1  GI:27291379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1286)
  AUTHORS   Komatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A.,
            Shi,Y., LaFleur,D.W., Wei,Y.-F., Ni,J., Florence,K.A., Young,P.,
            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H. and
            Mucenski,M.
  TITLE     Secreted protein HNFGF20
  JOURNAL   Patent: US 6476195-A 124 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .1286
                     /organism="unknown"
BASE COUNT      357 a    264 c    296 g    368 t      1 others
ORIGIN

  Query Match           97.3%;  Score 1222.8;  DB 6;  Length 1286;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-207;
  Matches 1246;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy          8 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCC 67
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          2 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG-C 60

Qy         68 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 120

Qy        128 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 180

Qy        188 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 240

Qy        248 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 307
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAAAAGGCGCA-CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 299

Qy        308 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTAC 367
              |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        300 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTAC 359

Qy        368 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 419

Qy        428 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 479

Qy        488 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 539

Qy        548 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 599

Qy        608 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 659

Qy        668 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 719

Qy        728 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 787
```

```
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          720 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 779

Qy          788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          780 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 839

Qy          848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          840 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 899

Qy          908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          900 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 959

Qy          968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTAAATCTAGC 1027
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          960 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTAAATCTAGC 1019

Qy         1028 ATTATTCATTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTTAGAATAC 1087
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1020 ATTATTCATTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTTAGAATAC 1079

Qy         1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1147
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1080 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1139

Qy         1148 TTTCTCTTAGTATAGCATTTTTAAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1207
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1140 TTTCTCTTAGTATAGCATTTTTAAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1199

Qy         1208 AAATGTTAAGAATTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1200 AAATGTTAAGAATTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1249


RESULT 9
BC014245
LOCUS       BC014245              1245 bp    mRNA    linear   PRI 12-SEP-2001
DEFINITION  Homo sapiens, Similar to RIKEN cDNA 1110014B07 gene, clone
            MGC:20766 IMAGE:4586039, mRNA, complete cds.
ACCESSION   BC014245
VERSION     BC014245.1  GI:15559789
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1245)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site:     http://www.nisc.nih.gov/
            Contact:      nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 30 Row: 1 Column: 18
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction.
FEATURES             Location/Qualifiers
     source          1..1245
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:20766 IMAGE:4586039"
                     /tissue_type="Kidney, renal cell adenocarcinoma"
                     /clone_lib="NIH_MGC_14"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             109..840
                     /codon_start=1
                     /product="Similar to RIKEN cDNA 1110014B07 gene"
                     /protein_id="AAH14245.1"
                     /db_xref="GI:15559790"
                     /translation="MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQ
                     REVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESW
                     TPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFT
                     FNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTC
                     SDYPKGDASTGWNSVSRIIIEELPK"
BASE COUNT      334 a    260 c    287 g    364 t
ORIGIN

  Query Match             96.8%;  Score 1217.2;  DB 9;  Length 1245;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-206;
  Matches 1219;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           36 AGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGT 95
                || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            7 AGGCTGCGGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGT 66

Qy           96 CTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCC 155
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           67 CTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCC 126

Qy          156 GCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCG 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          127 GCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCG 186

Qy          216 CCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAG 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          187 CCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAG 246

Qy          276 GTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGAC 335
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          247 GTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGAC 306

Qy          336 GGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTC 395
                |||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db          307 GGGAGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTC 366

Qy          396 AAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC 455
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          367 AAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC 426

Qy          456 AAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGT 515
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          427 AAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGT 486

Qy          516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          487 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 546

Qy          576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          547 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 606
```

```
Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 666

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 726

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 786

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 846

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 906

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 966

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1026

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1086

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1146

Qy       1176 ATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT 1235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 ATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT 1206

Qy       1236 TAAATAAAAATTATTTCCAACA 1257
              |||||||||||||||||||||
Db       1207 TAAATAAAAATTATTTCCAACA 1228


RESULT 10
AY136825
LOCUS       AY136825               1221 bp    mRNA    linear   PRI 01-DEC-2002
DEFINITION  Homo sapiens collagen triple helix repeat-containing protein 1
            (CTHRC1) mRNA, complete cds.
ACCESSION   AY136825
VERSION     AY136825.1  GI:25989620
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1221)
  AUTHORS   Lehnert,W., Moore,D.P., Harmon,K.J., Mancini,M.L. and Lindner,V.
  TITLE     Expression of the novel collagen triple helix repeat-containing
            gene (Cthrc1) suggests functions in multiple organ systems
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1221)
  AUTHORS   Lindner,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-2002) Center for Molecular Medicine, Maine
            Medical Center Research Institute, 81 Research Drive, Scarborough,
            ME 04074, USA
FEATURES             Location/Qualifiers
     source          1. .1221
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="8"
                     /tissue_type="aorta smooth muscle"
     gene            1. .1221
                     /gene="CTHRC1"
     CDS             104. .835
                     /gene="CTHRC1"
                     /note="matrix protein"
                     /codon_start=1
                     /product="collagen triple helix repeat-containing protein
                     1"
                     /protein_id="AAN15749.1"
                     /db_xref="GI:25989621"
                     /translation="MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQ
                     REVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESW
                     TPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFT
                     FNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTC
                     SDYPKGDASTGWNSVSRIIIEELPK"
BASE COUNT      316 a    258 c    285 g    362 t
ORIGIN
```

Query Match 95.4%; Score 1198.8; DB 9; Length 1221;
Best Local Similarity 99.8%; Pred. No. 2.7e-203;
Matches 1211; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy         43 GGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCC 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCC 68

Qy        103 GCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCT 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCT 128

Qy        163 CCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGA 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGA 188

Qy        223 GCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGG 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGG 248

Qy        283 ACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCC 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCC 308

Qy        343 CTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAG 402
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CTGGGGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAG 368

Qy        403 AAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGT 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGT 428

Qy        463 GTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTA 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTA 488

Qy        523 CAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAAT 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAAT 548

Qy        583 GCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGAC 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGAC 608

Qy        643 CTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAA 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAA 668

Qy        703 TTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAG 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 TTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAG 728
```

```
Qy        763 TGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTG 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTG 788

Qy        823 GATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 GATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT 848

Qy        883 CATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAAT 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 CATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAAT 908

Qy        943 AAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTG 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 AAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTG 968

Qy       1003 ATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAA 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 ATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAA 1028

Qy       1063 TATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTT 1122
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1029 TA-TTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTT 1087

Qy       1123 GGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAA 1182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1088 GGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAA 1147

Qy       1183 AGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAA 1242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1148 AGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAA 1207

Qy       1243 AAATTATTTCCAAC 1256
              ||||||||||||||
Db        1208 AAATTATTTCCAAC 1221
```

RESULT 11
AF395488

```
LOCUS       AF395488               1215 bp    mRNA    linear   PRI 07-JAN-2003
DEFINITION  Homo sapiens NTMC1 mRNA, complete cds.
ACCESSION   AF395488
VERSION     AF395488.1  GI:27525623
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1215)
  AUTHORS   Sanuki,N., Fujiki,K., Kanai,A., Tanaka,Y. and Iwata,T.
  TITLE     Novel polypeptide found in human cornea cDNA library
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1215)
  AUTHORS   Sanuki,N., Fujiki,K., Kanai,A., Tanaka,Y. and Iwata,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) National Center for Sensory Organs,
            National Tokyo Medical Center, 2-5-1 Higashigaoka, Meguro, Tokyo
            152-8902, Japan
FEATURES             Location/Qualifiers
     source          1. .1215
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             121. .819
                     /codon_start=1
                     /product="NTMC1"
                     /protein_id="AAO17919.1"
                     /db_xref="GI:27525624"
                     /translation="MWPPGRSITVKLREKTVSRKLEMNGPSAFQGLICGKYNGMCLQG
                     PAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNY
                     GIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEA
                     IIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNS
                     VSRIIIEELPIYML"
```

```
BASE COUNT      361 a    207 c    266 g    381 t
ORIGIN
```

Query Match 76.7%; Score 964.6; DB 9; Length 1215;
Best Local Similarity 99.6%; Pred. No. 1.2e-161;
Matches 967; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        287 GTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGG 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGG 287

Qy        347 GGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAA 406
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAA 347

Qy        407 GGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTC 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTC 407

Qy        467 ATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAA 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 ATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAA 467

Qy        527 GATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAG 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAG 527

Qy        587 AAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCT 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCT 587

Qy        647 TCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAA 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAA 647

Qy        707 TATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 TATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGA 707

Qy        767 TGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 TGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATG 767

Qy        827 GAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATT 886
              ||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db        768 GAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAATATATATGCTTTAATTTTCATT 827

Qy        887 TGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGT 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        828 TGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGT 887

Qy        947 TTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTT 1006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        888 TTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTT 947

Qy       1007 CACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATT 1066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        948 CACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATT 1007

Qy       1067 TTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAA 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1008 TTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAA 1067

Qy       1127 TATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCT 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1068 TATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCT 1127

Qy       1187 ACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAAT 1246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1128 ACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAAT 1187

Qy       1247 TATTTCCAACA 1257
              ||||||||||||
```

```
Db       1188 TATTTCCAACA 1198


RESULT 12
AX285214/c
LOCUS       AX285214                860 bp    DNA     linear   PAT 20-NOV-2001
DEFINITION  Sequence 1019 from Patent WO0179556.
ACCESSION   AX285214
VERSION     AX285214.1  GI:17045902
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lillie,J., Brown,J.L., Bolt,A. and van Huffel,C.
  TITLE     Novel genes, compositions and methods for the identification,
            assessment, prevention, and therapy of human cancers
  JOURNAL   Patent: WO 0179556-A 1019 25-OCT-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      315 a    149 c    127 g    259 t     10 others
ORIGIN

  Query Match           63.1%;  Score 793;  DB 6;  Length 860;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-131;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        465 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        828 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 769

Qy        525 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 709

Qy        585 AGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 AGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 649

Qy        645 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 589

Qy        705 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 529

Qy        765 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 469

Qy        825 TGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCA 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 TGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCA 409

Qy        885 TTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAA 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAA 349

Qy        945 GTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGAT 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGAT 289

Qy       1005 TTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 TTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATA 229

Qy       1065 TTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGG 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 TTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGG 169

Qy       1125 AATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAG 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 AATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAG 109

Qy       1185 CTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAA 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 CTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAA 49

Qy       1245 ATTATTTCCAACA 1257
              |||||||||||||
Db         48 ATTATTTCCAACA 36


RESULT 13
BD006704
LOCUS       BD006704                732 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel polypeptide.
ACCESSION   BD006704
VERSION     BD006704.1  GI:18635075
KEYWORDS    JP 2001029090-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Ito,Y., Mogi,S., Tanaka,H., Okubo,S. and Ogi,K.
  TITLE     Novel polypeptide
  JOURNAL   Patent: JP 2001029090-A 7 06-FEB-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001029090-A/7
            PD   06-FEB-2001
            PF   19-MAY-2000 JP 2000147530
            PR
            PI   YASUAKI ITO,SHINICHI MOGI,HIDEYUKI TANAKA,SHOICHI OKUBO, PI
            KAZUHIRO OGI
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
            PC   A61P1/00,
            PC   A61P5/00,A61P9/00,A61P11/00,A61P25/00,A61P25/18,A61P31/00, PC
             A61P35/00,
            PC   A61P37/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,G01N33/50,
            PC   G01N33/566//
            PC   C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/08,(C12P21/02, PC
            C12R1:91),
            PC   (C12N5/10,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
            PC   C12N5/00,
            PC   (C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .732
            FT   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      184 a    163 c    205 g    180 t
ORIGIN

  Query Match           58.0%;  Score 728.8;  DB 6;  Length 732;
  Best Local Similarity  99.7%;  Pred. No. 1e-119;
  Matches  730;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 ATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTG 60

Qy        198 CTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCG 120
```

```
Qy        258 CAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCA 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCA 180

Qy        318 GGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATC 377
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        181 GGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGATC 240

Qy        378 CCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAG 300

Qy        438 TCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTT 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTT 360

Qy        498 GGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTG 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTG 420

Qy        558 TTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACA 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACA 480

Qy        618 TTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAA 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAA 540

Qy        678 GGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTT 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTT 600

Qy        738 TGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGAT 797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGAT 660

Qy        798 TACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAA 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAA 720

Qy        858 CTACCAAAATAA 869
              ||||||||||||
Db        721 CTACCAAAATAA 732
```

```
RESULT 14
AX375790/c
LOCUS       AX375790                683 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 3 from Patent WO0173031.
ACCESSION   AX375790
VERSION     AX375790.1  GI:19170293
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J. and Stolk,J.A.
  TITLE     Compositions and methods for the therapy and diagnosis of ovarian
            cancer
  JOURNAL   Patent: WO 0173031-A 3 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      256 a    118 c    108 g    199 t      2 others
ORIGIN

  Query Match           54.3%;  Score 682.2;  DB 6;  Length 683;
  Best Local Similarity 99.7%;  Pred. No. 1.9e-111;
  Matches  681;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAARGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

```
RESULT 15
AR280558/c
LOCUS       AR280558                683 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 63 from patent US 6518237.
ACCESSION   AR280558
VERSION     AR280558.1  GI:29716028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   Yuqiu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.
  TITLE     Compositions for treatment and diagnosis of breast cancer and
            methods for their use
  JOURNAL   Patent: US 6518237-A 63 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="unknown"
BASE COUNT      255 a    118 c    107 g    200 t      3 others
ORIGIN

  Query Match           54.2%;  Score 681.8;  DB 6;  Length 683;
```

Best Local Similarity 99.6%; Pred. No. 2.3e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

Search completed: August 20, 2003, 13:48:00
Job time : 4791 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 11:55:54 ; Search time 381 Seconds
(without alignments)
8906.020 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1257	100.0	1257	21	AAA37144	Human PRO1550 cDNA
2	1257	100.0	1257	22	AAS46107	Human DNA encoding
3	1257	100.0	1257	22	AAF92118	Human PRO1550 cDNA
4	1257	100.0	1257	22	AAF54507	Probe #60 used in
5	1257	100.0	1257	24	ABS74438	Human cDNA encodin
6	1257	100.0	1257	24	ABL95683	Human angiogenesis
7	1257	100.0	1257	24	AAD32717	Human tumour-assoc
8	1257	100.0	1257	24	ABL88194	Human PRO1550 cDNA
9	1257	100.0	1257	25	ACA57865	Human PRO1550 cDNA
10	1257	100.0	1257	25	ACA58870	cDNA encoding huma
11	1257	100.0	1257	25	ACA60423	Novel human secret
12	1257	100.0	1257	25	ACA63433	cDNA encoding huma
13	1257	100.0	1257	25	ABX98335	Human cDNA encodin
14	1257	100.0	1257	25	ABX98837	Novel human secret
15	1257	100.0	1257	25	ACA05882	Human secreted/tra
16	1257	100.0	1257	25	ABX12411	cDNA encoding huma
17	1257	100.0	1257	25	ABX97926	Human PRO polynucl
18	1257	100.0	1257	25	ABX78710	Human PRO polynucl
19	1257	100.0	1257	25	ABX75723	Human cDNA encodin
20	1257	100.0	1257	25	ABX76928	Human PRO polynucl
21	1257	100.0	1257	25	ABX16768	Human cDNA encodin
22	1253.8	99.7	1265	25	ABX63682	Human cDNA #682 di
23	1253.8	99.7	1284	24	ABT07711	Breast cancer-asso
24	1253.8	99.7	1284	25	ACC51043	Human bladder canc
25	1253.8	99.7	1284	25	ABX76336	Lung cancer-associ
26	1253.8	99.7	1340	24	ABS76436	cDNA encoding huma
c 27	1250.6	99.5	1295	22	AAH99687	Human protein enco
28	1236.8	98.4	1257	21	AAA75110	cDNA encoding a hu
29	1236.8	98.4	1257	24	ABS76434	cDNA encoding huma
30	1236.8	98.4	1257	25	ACC50329	Breast cancer asso
31	1234.4	98.2	1352	25	ABT31900	Human breast cance
32	1231.6	98.0	1320	24	ABV99139	Human pancreatic c
33	1231.6	98.0	1342	21	AAA26424	Human secreted pro
34	1222.8	97.3	1286	21	AAA26456	Human secreted pro
35	1199.8	95.4	1220	24	ABN86481	Human REMODELIN po
36	1199.8	95.4	1220	25	ABX11341	Human REMODELIN cD
37	1197	95.2	1288	20	AAV84525	Human secreted pro
38	1197	95.2	1288	22	ABA83308	Human secreted pro
39	1125.8	89.6	1131	24	ABV95046	Human pancreatic c
40	969.2	77.1	1177	24	ABS76435	cDNA encoding huma
41	910.6	72.4	1173	25	ABX63719	Human cDNA #719 di
42	826	65.7	837	24	ABV99145	Human pancreatic c
43	826	65.7	837	24	ABS64030	Human breast tumou
44	826	65.7	837	24	ABS64031	Human breast tumou
45	826	65.7	837	25	ABT33242	Human tumour-relat

ALIGNMENTS

RESULT 1
AAA37144
ID AAA37144 standard; cDNA; 1257 BP.
XX
AC AAA37144;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1550 cDNA sequence SEQ ID NO:430.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.

PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR P-PSDB; AAY99462.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 2; Fig 245; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 21; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

```
Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 2
AAS46107
ID AAS46107 standard; cDNA; 1257 BP.
XX
AC AAS46107;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #183.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX

```
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   P-PSDB; AAU29206.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 2; Fig 365; 774pp; English.
XX
CC   Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC   primers for PRO polypeptides of the invention. The sequences of the
CC   invention can be used to detect the presence of a tumour in a mammal by
CC   comparing the level of expression of a PRO polypeptide in a test sample
CC   of cells from the animal and a control sample of normal cells, whereby a
CC   higher level of expression in the test sample indicates the presence of a
CC   tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC   pigs, goats and rabbits but are preferably human. The polypeptides can be
CC   used to stimulate tumour necrosis factor (TNF) alpha release from human
CC   blood, when contacted with it. A specific polypeptide can be used to
CC   stimulate the proliferation or differentiation of chondrocyte cells. The
CC   PRO proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

  Query Match           100.0%;  Score 1257;  DB 22;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 3
AAF92118
ID   AAF92118 standard; cDNA; 1257 BP.
XX
AC   AAF92118;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1550 cDNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
```

```
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   P-PSDB; AAB87586.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping. -
XX
PS   Claim 2; Fig 121; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping.
XX
SQ   Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

  Query Match           100.0%;  Score 1257;  DB 22;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 4
AAF54507
ID   AAF54507 standard; DNA; 1257 BP.
XX
AC   AAF54507;
XX
DT   02-APR-2001  (first entry)
XX
DE   Probe #60 used in the identification of proteins.
XX
KW   Secreted; transmembrane; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US04342.
XX
PR   23-JUN-1999;   99US-0141037.
```

```
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   01-SEP-1999;   99WO-US20111.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI   Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI   Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI   Watanabe CK, Williams PM, Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy -
XX
PS   Example 124; Page 489; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of
CC   anti-sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents.
CC   The nucleic acids may also be used in gene therapy.
XX
SQ   Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

  Query Match           100.0%;  Score 1257;  DB 22;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 5
ABS74438
ID   ABS74438 standard; cDNA; 1257 BP.
XX
AC   ABS74438;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1550.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-0006867.
XX
```

PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-064215P.
PR 22-APR-1998; 98US-082797P.
PR 29-APR-1998; 98US-083495P.
PR 15-MAY-1998; 98US-085579P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 11-JUN-1998; 98US-088863P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089514P.
PR 16-SEP-1998; 98WO-US19330.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21194.
PR 22-DEC-1999; 99WO-US30720.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32378.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR P-PSDB; ABG95911.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating
PT sports-related joint problems, osteoarthritis or rheumatoid arthritis
XX
PS Claim 2; Fig 121; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing
CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
CC an extracellular domain of the proteins with their associated signal
CC peptide or lacking its associated signal peptide. Also included are
CC the nucleic acids encoding the proteins, vectors, host cells,
CC fusion proteins and antibodies which specifically bind to the proteins.
CC The proteins are useful for detecting a polypeptide designated as A, B, C
CC or D in a sample suspected of containing an A, B, C or D polypeptide,
CC by contacting the sample with a polypeptide designated as E, F, G, H or
CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
CC or D/I polypeptide conjugate in the sample, where the formation of the
CC conjugate is indicative of the presence of an A, B, C or D polypeptide
CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
CC polypeptide. The sample comprises a cell suspected of expressing the A,
CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
CC a detectable label or is attached to a solid support. The proteins are
CC useful for linking a bioactive molecule to a cell expressing a
CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
CC against them are useful for modulating a biological activity of a cell
CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
CC I. The cell is killed. The proteins are useful for identifying
CC agonists or antagonists, for the preparation of a medicament useful in
CC the treatment of a condition which is responsive to the proteins, as
CC molecular weight markers for protein electrophoresis purposes, and as
CC therapeutic agents for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.
CC Nucleic acids encoding the proteins are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of anti-sense RNA and
CC DNA, for the preparation of the proteins, to generate transgenic or
CC knockout animals which are useful in the development and screening of
CC therapeutic useful reagents, for chromosome identification, and in gene
CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic
CC assay and for affinity purification of the protein from recombinant
CC cell culture natural sources. The present sequence encodes a novel
CC secreted or transmembrane protein of the invention.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 24; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 6
ABL95683
ID ABL95683 standard; cDNA; 1257 BP.
XX
AC ABL95683;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO1550 SEQ ID NO: 245.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-PSDB; ABB95545.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 1; Fig 245; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

```
  Query Match             100.0%;  Score 1257;  DB 24;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
```

```
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 7
AAD32717
ID   AAD32717 standard; cDNA; 1257 BP.
XX
AC   AAD32717;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human tumour-associated antigenic target-170 (TAT170) cDNA.
XX
KW   Human; tumour-associated antigenic target-170; TAT170; cytostatic;
KW   gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             138..869
FT                   /*tag= a
FT                   /product= "Human TAT170 protein"
FT   sig_peptide     138..227
FT                   /*tag= b
FT   mat_peptide     228..866
FT                   /*tag= c
FT                   /product= "Mature TAT170 protein"
XX
PN   WO200216602-A2.
XX
PD   28-FEB-2002.
XX
PF   23-AUG-2001; 2001WO-US26626.
XX
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Goddard A,  Godowski PJ,  Gurney AL,  Polakis P;
PI   Williams PM,  Wood WI,  Wu TD,  Zhang Z;
XX
DR   WPI; 2002-292065/33.
DR   P-PSDB; AAE20462.
XX
PT   New antibodies that bind tumor-associated antigenic target (TAT)
PT   polypeptides, useful for treating and diagnosing tumor (e.g. breast,
PT   lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
PT   pigs, goats, rabbits or humans  -
XX
PS   Claim 1; Fig 2; 124pp; English.
XX
CC   The present invention relates to an isolated antibody that binds to
CC   tumor-associated antigenic target (TAT) polypeptide. The antibody is
CC   used for treating and diagnosing tumours (e.g. breast, lung, liver or
CC   stomach tumours) in mammals, e.g. dogs, cats, cattle, horses, sheep,
CC   pigs, goats, rabbits, or preferably humans. The antibody may also be
CC   used in antibody-dependent enzyme mediated prodrug therapy (ADEPT).
CC   The antibody is also useful for the therapeutic treatment or for the
CC   diagnostic detection of cancer. TAT cDNA is useful in gene therapy.
CC   The present sequence is human TAT170 cDNA designated DNA76393-1664.
XX
SQ   Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;
```

```
Query Match             100.0%;  Score 1257;  DB 24;  Length 1257;
Best Local Similarity   100.0%;  Pred. No. 1.7e-251;
Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 8
ABL88194
ID ABL88194 standard; cDNA; 1257 BP.
XX
AC ABL88194;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1550 cDNA sequence SEQ ID NO:245.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.

```
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   P-PSDB; ABB84939.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 2; Fig 245; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

  Query Match           100.0%;  Score 1257;  DB 24;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 9
ACA57865
ID   ACA57865 standard; cDNA; 1257 BP.
XX
AC   ACA57865;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Human PRO1550 cDNA.
XX
KW   Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood; gene;
KW   tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW   differentiation; tumour; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   US2003036143-A1.
XX
```

PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.

```
PR   26-JUN-1998;   98US-090862P.
PR   26-JUN-1998;   98US-090863P.
PR   26-JUN-1998;   98US-091010P.
PR   01-JUL-1998;   98US-091359P.
PR   01-JUL-1998;   98US-091544P.
PR   02-JUL-1998;   98US-091478P.
PR   02-JUL-1998;   98US-091486P.
PR   02-JUL-1998;   98US-091626P.
PR   02-JUL-1998;   98US-091628P.
PR   02-JUL-1998;   98US-091632P.
PR   24-JUL-1998;   98US-094006P.
PR   04-AUG-1998;   98US-095282P.
PR   10-AUG-1998;   98US-095998P.
PR   10-AUG-1998;   98US-096012P.
PR   17-AUG-1998;   98US-096757P.
PR   17-AUG-1998;   98US-096766P.
PR   17-AUG-1998;   98US-096867P.
PR   17-AUG-1998;   98US-096891P.
PR   17-AUG-1998;   98US-096897P.
PR   18-AUG-1998;   98US-096949P.
PR   18-AUG-1998;   98US-096959P.
PR   18-AUG-1998;   98US-097022P.
PR   26-AUG-1998;   98US-097952P.
PR   26-AUG-1998;   98US-097954P.
PR   26-AUG-1998;   98US-097955P.
PR   26-AUG-1998;   98US-097971P.
PR   26-AUG-1998;   98US-097974P.
PR   26-AUG-1998;   98US-098014P.
PR   01-SEP-1998;   98US-098716P.
PR   01-SEP-1998;   98US-098723P.
PR   02-SEP-1998;   98US-098803P.
PR   02-SEP-1998;   98US-098821P.
PR   02-SEP-1998;   98US-098843P.
PR   09-SEP-1998;   98US-099602P.
PR   10-SEP-1998;   98US-099741P.
PR   10-SEP-1998;   98US-099754P.
PR   10-SEP-1998;   98US-099763P.
PR   10-SEP-1998;   98US-099812P.

  Query Match           100.0%;  Score 1257;  DB 25;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTTCTCTTAGTATAGCATTTTTAAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTTCTCTTAGTATAGCATTTTTAAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 10
ACA58870
ID   ACA58870 standard; cDNA; 1257 BP.
XX
AC   ACA58870;
XX
DT   10-JUN-2003  (first entry)
XX
DE   cDNA encoding human secreted polypeptide PRO1550.
XX
KW   Human; ss; gene; gene therapy; tumour; cancer.
XX
OS   Homo sapiens.
XX
PN   US2003013855-A1.
XX
PD   16-JAN-2003.
XX
```

PF 03-MAY-2002; 2002US-0063616.
XX
PR 30-DEC-1998; 98KR-0062142.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 21-MAR-2000; 2000WO-US07532.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 14-MAY-1999; 99US-0311832.
PR 25-AUG-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 15-SEP-1999; 99US-0397342.
PR 18-OCT-1999; 99US-0403297.
PR 12-NOV-1999; 99US-0423844.
PR 22-AUG-2000; 2000US-0644848.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 08-NOV-2000; 2000US-0709238.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 30-MAY-2001; 2001US-0870574.
PR 05-JUN-2001; 2001US-0874503.
PR 29-JUN-2001; 2001US-0869599.
PR 18-JUL-2001; 2001US-0908827.
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330485/31.
DR P-PSDB; ABU71566.
XX
PT New isolated antibody specifically binding a PRO polypeptide, useful
PT for the preparation of a medicament for treating disorders with the
PT aberrant expression or activity of the PRO polypeptide, such as tumor
PT conditions and cancer -
XX
PS Example 4; Page 193-194; 406pp; English.
XX
CC The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention.
XX

SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 25; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
```

```
Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 11
ACA60423
ID ACA60423 standard; cDNA; 1257 BP.
XX
AC ACA60423;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1550 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; gene; ss.
KW chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003018183-A1.
XX
PD 23-JAN-2003.
XX
PF 01-MAY-2002; 2002US-0063512.
XX
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR P-PSDB; ABU72012.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody -
XX
PS Disclosure; Fig 121; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human
CC secreted and transmembrane PRO poypeptide.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

```
  Query Match             100.0%;  Score 1257;  DB 25;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
```

```
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 12
ACA63433
ID ACA63433 standard; cDNA; 1257 BP.
XX
AC ACA63433;
XX
DT 13-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #61.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003023042-A1.
XX
PD 30-JAN-2003.
XX
PF 01-MAY-2002; 2002US-0063502.
XX
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-331484/31.
DR P-PSDB; ABU72169.
XX
PT Novel monoclonal antibody that binds to secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and
PT also for treating conditions responsive to the antibody
XX
PS Disclosure; Fig 121; 408pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a
CC medicament useful in the treatment of a condition responsive to
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells,
CC tissues or serum, and for affinity purification of PRO from
CC recombinant cell culture or natural sources. ACA63373-ACA63456
CC represent cDNA sequences encoding the human PRO polypeptides of
CC the invention.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

Query Match 100.0%; Score 1257; DB 25; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 13
ABX98335
ID ABX98335 standard; cDNA; 1257 BP.
XX
AC ABX98335;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.
XX
OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.

PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.

Query Match 100.0%; Score 1257; DB 25; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 14
ABX98837
ID   ABX98837 standard; cDNA; 1257 BP.
XX
AC   ABX98837;
XX
DT   20-MAY-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1550 cDNA.
XX
KW   Human; secreted protein; transmembrane protein; cytostatic;
KW   gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW   adrenal tumour; lung tumour; colon tumour; breast tumour;
KW   prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003036157-A1.
XX
PD   20-FEB-2003.
XX
PF   02-JUL-2002; 2002US-0188769.
XX
PR   16-SEP-1998;   98WO-US19330.
PR   07-OCT-1998;   98WO-US21141.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28551.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   29-AUG-2001; 2001WO-US27099.
PR   18-SEP-1997;   97US-059263P.
PR   18-SEP-1997;   97US-059266P.
PR   17-OCT-1997;   97US-062250P.
PR   21-OCT-1997;   97US-063486P.
PR   24-OCT-1997;   97US-063120P.
PR   24-OCT-1997;   97US-063121P.
PR   28-OCT-1997;   97US-063540P.
PR   28-OCT-1997;   97US-063541P.
PR   28-OCT-1997;   97US-063544P.
PR   28-OCT-1997;   97US-063564P.
PR   29-OCT-1997;   97US-063734P.
PR   31-OCT-1997;   97US-063870P.
PR   31-OCT-1997;   97US-064103P.
PR   13-NOV-1997;   97US-065311P.
PR   21-NOV-1997;   97US-066120P.
PR   24-NOV-1997;   97US-066466P.
PR   24-NOV-1997;   97US-066772P.
PR   11-DEC-1997;   97US-069335P.
PR   12-DEC-1997;   97US-069425P.
PR   17-DEC-1997;   97US-069870P.
PR   18-DEC-1997;   97US-068017P.
PR   10-MAR-1998;   98US-077450P.
PR   11-MAR-1998;   98US-077632P.
PR   11-MAR-1998;   98US-077649P.
PR   20-MAR-1998;   98US-078886P.
PR   20-MAR-1998;   98US-078939P.
PR   27-MAR-1998;   98US-079664P.
PR   27-MAR-1998;   98US-079786P.
PR   31-MAR-1998;   98US-080107P.
PR   31-MAR-1998;   98US-080194P.
PR   01-APR-1998;   98US-080327P.
PR   01-APR-1998;   98US-080333P.
PR   08-APR-1998;   98US-081049P.
PR   08-APR-1998;   98US-081070P.
PR   09-APR-1998;   98US-081195P.
PR   15-APR-1998;   98US-081838P.
PR   21-APR-1998;   98US-082568P.
PR   21-APR-1998;   98US-082569P.
PR   22-APR-1998;   98US-082704P.
PR   22-APR-1998;   98US-082797P.
PR   28-APR-1998;   98US-083322P.
PR   29-APR-1998;   98US-083495P.
PR   29-APR-1998;   98US-083496P.
PR   29-APR-1998;   98US-083499P.
PR   29-APR-1998;   98US-083559P.
PR   05-MAY-1998;   98US-084366P.
PR   06-MAY-1998;   98US-084414P.
PR   07-MAY-1998;   98US-084639P.
PR   07-MAY-1998;   98US-084640P.
PR   07-MAY-1998;   98US-084643P.
PR   15-MAY-1998;   98US-085579P.
PR   15-MAY-1998;   98US-085580P.
PR   15-MAY-1998;   98US-085582P.
PR   15-MAY-1998;   98US-085700P.
PR   18-MAY-1998;   98US-086023P.
PR   22-MAY-1998;   98US-086392P.
PR   22-MAY-1998;   98US-086486P.
PR   28-MAY-1998;   98US-087098P.
PR   28-MAY-1998;   98US-087208P.
PR   02-JUN-1998;   98US-087609P.
PR   02-JUN-1998;   98US-087759P.
PR   03-JUN-1998;   98US-087827P.
PR   04-JUN-1998;   98US-088025P.
PR   04-JUN-1998;   98US-088028P.
PR   04-JUN-1998;   98US-088029P.
PR   04-JUN-1998;   98US-088033P.
PR   04-JUN-1998;   98US-088326P.
PR   05-JUN-1998;   98US-088167P.
PR   05-JUN-1998;   98US-088202P.
PR   05-JUN-1998;   98US-088212P.
PR   05-JUN-1998;   98US-088217P.
PR   09-JUN-1998;   98US-088655P.
PR   10-JUN-1998;   98US-088722P.
```

PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.

Query Match 100.0%; Score 1257; DB 25; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 15
ACA05882
ID ACA05882 standard; cDNA; 1257 BP.
XX
AC ACA05882;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #183.
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-0194423.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 03-MAR-1999; 99US-0254311.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 18-OCT-1999; 99US-0403297.
PR 12-NOV-1999; 99US-0423844.
PR 22-AUG-2000; 2000US-0644848.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 08-NOV-2000; 2000US-0709238.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 05-JUN-2001; 2001US-0874503.
PR 18-JUL-2001; 2001US-0908827.
PR 30-JUL-2001; 2001US-0918585.
PR 06-AUG-2001; 2001US-0924419.
PR 13-AUG-2001; 2001US-0929404.
PR 16-AUG-2001; 2001US-0931836.
PR 28-AUG-2001; 2001US-0941992.
PR 04-SEP-2001; 2001US-0946374.
PR 15-JAN-2002; 2002US-0052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332039/31.
DR P-PSDB; ABU67588.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids,
PT useful in gene therapy, in chromosome and gene mapping, as chromosome
PT markers, in tissue typing, and in chromosome identification -
XX
PS Claim 2; Fig 365; 706pp; English.
XX
CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention.
XX
SQ Sequence 1257 BP; 324 A; 264 C; 299 G; 370 T; 0 other;

```
  Query Match           100.0%;  Score 1257;  DB 25;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-251;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
```

```
Qy        61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy       121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

Search completed: August 20, 2003, 13:54:28
Job time : 385 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 12:23:44 ; Search time 2967 Seconds
(without alignments)
10296.841 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1252.2	99.6	1288	11	BC021025	BC021025 Homo sapi
	2	999	79.5	1201	9	AL532456	AL532456 AL532456
c	3	951.8	75.7	1190	9	AL575307	AL575307 AL575307
c	4	946.6	75.3	1201	9	AL564395	AL564395 AL564395
	5	914.2	72.7	1201	9	AL551834	AL551834 AL551834
	6	861.6	68.5	1201	13	BX387691	BX387691 BX387691
c	7	842.6	67.0	1201	13	BX387690	BX387690 BX387690
	8	842.2	67.0	1132	12	BM560093	BM560093 AGENCOURT
	9	815.2	64.9	903	12	BI763295	BI763295 603047656
	10	811.2	64.5	887	9	AL544722	AL544722 AL544722
	11	739.4	58.8	851	13	BQ425266	BQ425266 AGENCOURT
	12	716.4	57.0	922	13	BQ425098	BQ425098 AGENCOURT
	13	705.4	56.1	1037	12	BM915926	BM915926 AGENCOURT
c	14	700.4	55.7	747	14	CA415410	CA415410 UI-H-EZ0-
c	15	695.6	55.3	796	12	BQ008675	BQ008675 UI-H-EI0-
	16	693.2	55.1	734	13	BX114800	BX114800 BX114800
c	17	691	55.0	723	14	CA431413	CA431413 UI-H-FG1-
c	18	690	54.9	724	12	BQ009009	BQ009009 UI-H-EI0-
c	19	682.2	54.3	716	14	CA413294	CA413294 UI-H-EZ0-
c	20	682	54.3	702	12	BQ010155	BQ010155 UI-H-ED0-
c	21	681.4	54.2	683	10	BE607413	BE607413 colonEST0
	22	681.4	54.2	683	10	BE607414	BE607414 colonEST0
c	23	679.8	54.1	837	9	AL570753	AL570753 AL570753
	24	679.6	54.1	949	9	AL553798	AL553798 AL553798
c	25	679	54.0	730	13	BU729033	BU729033 UI-E-CQ1-
	26	678.2	54.0	1099	12	BM915288	BM915288 AGENCOURT
	27	672.6	53.5	986	13	BQ648112	BQ648112 AGENCOURT
	28	672.4	53.5	1046	13	BX386416	BX386416 BX386416
	29	672.2	53.5	902	13	BQ424201	BQ424201 AGENCOURT
	30	658.2	52.4	1161	11	AK003674	AK003674 Mus muscu
c	31	655.4	52.1	723	12	BQ005403	BQ005403 UI-H-EI1-
	32	651.6	51.8	1168	11	AK076498	AK076498 Mus muscu
c	33	649.8	51.7	671	13	BU624465	BU624465 UI-H-FG1-
	34	641.8	51.1	688	10	BE387335	BE387335 601276538
	35	641	51.0	688	10	BE896915	BE896915 601439437
c	36	637.4	50.7	1045	13	BX386415	BX386415 BX386415
c	37	633.8	50.4	654	13	BU624261	BU624261 UI-H-FG1-
c	38	629.2	50.1	956	9	AL553771	AL553771 AL553771
	39	608.8	48.4	798	14	CB959810	CB959810 AGENCOURT
	40	606.2	48.2	1023	10	BG421228	BG421228 602451719
	41	597	47.5	849	14	CB201936	CB201936 AGENCOURT
c	42	581.4	46.3	610	12	BQ013605	BQ013605 UI-1-BC1p
	43	577	45.9	814	14	CB991371	CB991371 AGENCOURT
c	44	569.6	45.3	617	13	BQ574527	BQ574527 UI-H-EZ1-
c	45	567.4	45.1	569	9	AW071610	AW071610 wt94b06.x

ALIGNMENTS

RESULT 1
BC021025
LOCUS BC021025 1288 bp mRNA linear HTC 03-JAN-2002
DEFINITION Homo sapiens, clone IMAGE:3617432, mRNA.
ACCESSION BC021025
VERSION BC021025.1 GI:18045042
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1288)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 24 Row: i Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: no cloning site / microdeletion.

```
FEATURES             Location/Qualifiers
     source          1. .1288
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3617432"
                     /tissue_type="Skin, melanotic melanoma."
                     /clone_lib="NIH_MGC_20"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
BASE COUNT      346 a    268 c    303 g    371 t
ORIGIN
```

Query Match 99.6%; Score 1252.2; DB 11; Length 1288;
Best Local Similarity 99.8%; Pred. No. 3.1e-198;
Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 65

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 125

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 185

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 245

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 305

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db        306 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTC 365

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 425

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 485

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 545

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 605

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 665

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 725

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 785

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        786 TTGGCACTTGTTCAGATTACCCAAAATGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 845

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 905

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 965

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1025

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1085

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1145

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1205

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1262
```

```
RESULT 2
AL532456
LOCUS       AL532456               1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL532456 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM014YN20 5-PRIME, mRNA sequence.
ACCESSION   AL532456
VERSION     AL532456.2  GI:31070288
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12795949.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DM014DG10QP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DM014DG10QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
                     /clone="CS0DM014YN20"
                     /tissue_type="FETAL LIVER"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL LIVER"
                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      328 a    229 c    264 g    351 t     29 others
ORIGIN

  Query Match             79.5%;  Score 999;  DB 9;  Length 1201;
  Best Local Similarity   96.2%;  Pred. No. 3.6e-156;
  Matches 1059;  Conservative   15;  Mismatches   20;  Indels    7;  Gaps    5;

Qy        140 GCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCT 199
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 GCGCCCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCT 119

Qy        200 GCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCA 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db        120 GCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGSGCA 179

Qy        260 GCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGG 319
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 G-TCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGG 238

Qy        320 AGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCC 379
              ||||||||||||||||||:|||||||||||||||  ||||||||||||||||||||||||
Db        239 AGTGCCTGGTCGAGACGGGMGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGATCCC 298

Qy        380 AGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTC 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 AGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTC 358

Qy        440 CTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGG 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 CTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGG 418

Qy        500 GAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTT 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTT 478

Qy        560 CAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATT 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 CAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATT 538

Qy        620 CAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGG 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGG 598

Qy        680 AAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTG 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 AAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTG 658

Qy        740 TGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTA 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 TGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTA 718

Qy        800 CCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACT 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 CCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACT 778

Qy        860 ACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGG 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGG 838

Qy        920 TTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAA 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 TTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAA 898

Qy        980 ATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTT 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 ATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTT 958

Qy       1040 GCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGT 1099
              ||||||||||||||||||:|||||||:|||||||||||||||:: ||||||||||||||||
Db        959 GCTTCAATCAAAAGTGGKTTCAATAWTTTTTTTAGTTGGTTWRGATACTTTCTTCATAGT 1018

Qy       1100 CACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTA 1159
              ||||| |:|||||||||||:|||||||||||||| ||||:||| ||||||||:|
Db       1019 CACAT--CTCTCAMCTATAATTTGGRATATTGTTGTGGTC-TTTGKTTTGTCTCTTAGKA 1075

Qy       1160 TAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAA 1219
              |||||||||:|||||||||||||||| :|||||||||:|||| ||  |||||||||
Db       1076 TAGCATTTTTWAAAAAATATAAAAGC-WCCAATCTTTKTACA--TTTGTAATGTTAAGAT 1132

Qy       1220 TTTTTTTTATATCTGTTAAAT 1240
              |||||:|| | |   : ||||
Db       1133 TTTTTWTTTTTTTAAWAAAAT 1153


RESULT 3
AL575307/c
LOCUS       AL575307               1190 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  AL575307 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI061YA20 3-PRIME, mRNA sequence.
ACCESSION   AL575307
VERSION     AL575307.2  GI:31313615
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1190)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12936346.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI061BA10NP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI061BA10NP1.
FEATURES             Location/Qualifiers
     source          1. .1190
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI061YA20"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      370 a    248 c    212 g    321 t     39 others
ORIGIN

  Query Match             75.7%;  Score 951.8;  DB 9;  Length 1190;
  Best Local Similarity   95.6%;  Pred. No. 2.5e-148;
  Matches  992;  Conservative    5;  Mismatches   38;  Indels    3;  Gaps    2;

Qy        199 TGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGC 258
              | |||: :    : || |   ||   ||  ||      ||| | ||||||||||||||||
Db       1037 TTCTGYTSTGCASTGCCCGCSCGTCGGCGCCTYTAGATCCCCAAGGGAAGCAAAAGGCGC 978
```

```
Qy        259 AGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAG 318
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        977 AGCTCCGGCAGAGGGAGGTGGT-GACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAG 919

Qy        319 GAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC 378
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        918 GAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGATCC 859

Qy        379 CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGT 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGT 799

Qy        439 CCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTG 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTG 739

Qy        499 GGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT 558
              |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        738 GGAAAATTGCGGAGTGTACATTKACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT 679

Qy        559 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACAT 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACAT 619

Qy        619 TCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAG 559

Qy        679 GAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTT 499

Qy        739 GTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATT 439

Qy        799 ACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAAC 858
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        438 ACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTGTCTCGCATCATTATTGAAGAAC 379

Qy        859 TACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATG 319

Qy        919 GTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTA 978
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        318 GTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTTAATGAAAAGCAAAGCTA 259

Qy        979 AATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTT 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTT 199

Qy       1039 TGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAG 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAG 139

Qy       1099 TCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGT 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 TCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGT 79

Qy       1159 ATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC--AATTTGTAAATGTTAA 1216
              |||||||||||||||||||||||||||||||||||||||||  |       ||| ||||
Db         78 ATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACCAACCNNNANAATNTTAA 19

Qy       1217 GAATTTTTTTTATATCTG 1234
              |||||| |||||||||:
Db         18 AAATTTTATTTATATCTD 1
```

RESULT 4
AL564395/c

```
LOCUS       AL564395               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL564395 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM014YN20 3-PRIME, mRNA sequence.
ACCESSION   AL564395
VERSION     AL564395.2  GI:31288373
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12914757.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DM014DG10NP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DM014DG10NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DM014YN20"
                     /tissue_type="FETAL LIVER"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL LIVER"
                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
BASE COUNT      346 a    249 c    238 g    336 t     32 others
ORIGIN
```

Query Match 75.3%; Score 946.6; DB 9; Length 1201;
Best Local Similarity 93.9%; Pred. No. 1.8e-147;
Matches 1028; Conservative 9; Mismatches 53; Indels 5; Gaps 5;

```
Qy        127 AGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCC 186
              || | | |: | |.|| || |||: || | | | ||||:| |         | |   |
Db       1091 AGAGGTGTACSGTCCGAATCCSGGGSRCCCCAGGCCCCCCSCYCCCCGCAGCGGYCGCGC 1032

Qy        187 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGA 246
              ||  | ||  |           ||||||||||||||| :|| ||||||||||| ||||
Db       1031 CTCTTGTGCTCTTCTGTGCAGCTCCCGCGCCGTCGAGC-SCTTTGAGATCCCCAA-GGGA 974

Qy        247 AGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTAC 306
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| ||
Db        973 AGCAAAAGGCGCAGCTCCGGCAGAGGGAGGT-GTGGACCTGTATAATGGAATGTGCTAAC 915

Qy        307 AAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTA 366
              |||||||||||||||||||||||||||||||||||||||||||| ||||  |||||||||
Db        914 AAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCAAATGGCATTCCGGGTA 855

Qy        367 CACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAA 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 CACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAA 795

Qy        427 GCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 GCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATG 735

Qy        487 GCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTC 546
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        734 GCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACARAGATGCGTTCAAATAGTGCTC 675
```

```
Qy        547 TAAGAGTTTTGTTCAGTGGCTCACTTCG-GCTAAAATGCAGAAATGCATGCTGTCAGCGT 605
              |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Db        674 TAAGAGTTTTGTTAAGTGGCTCACTTCGCGCTAAAATGCAGAAATGCATGCTGTCAGCGT 615

Qy        606 TGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATT 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 TGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATT 555

Qy        666 TATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCT 725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 TATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCT 495

Qy        726 GTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGC 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 GTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGC 435

Qy        786 ACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        434 ACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTKTCTCGCATC 375

Qy        846 ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATT 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATT 315

Qy        906 ATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATG 965
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        314 ATGCCTTGGAATGGTTTACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATG 255

Qy        966 AAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTA 1025
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        254 AAAAGCAAAGCTAAATATGTTTMCAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTA 195

Qy       1026 GCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAAT 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAAT 135

Qy       1086 ACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGT 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGT 75

Qy       1146 TTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTT 1205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |:
Db          74 TTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAA-TW 16

Qy       1206 GTAAATGTTAAGAAT 1220
              |||||:|||||||||
Db          15 GTAAAKGTTAAGAAT 1
```

RESULT 5
AL551834

```
LOCUS       AL551834               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL551834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI061YA20 5-PRIME, mRNA sequence.
ACCESSION   AL551834
VERSION     AL551834.2  GI:31273650
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12890161.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI061BA10QP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI061BA10QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI061YA20"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      307 a    258 c    287 g    327 t     22 others
ORIGIN
```

```
  Query Match             72.7%;  Score 914.2;  DB 9;  Length 1201;
  Best Local Similarity   94.8%;  Pred. No. 4.4e-142;
  Matches  983; Conservative    5;  Mismatches   40;  Indels    9;  Gaps    4;

Qy         45 CGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGC 104
              |||  |||||||||||||  |   |||||||||||||||||||||||||||||||||||
Db         61 CGGGATCGGAGCGCGGCGGNACAGNACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGC 120

Qy        105 CTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCC 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCC 180

Qy        165 CCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGC 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGC 240

Qy        225 GCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGAC 284
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        241 GCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCA-CTCCGGCAGAGGGAGGTGGTGGAC 299

Qy        285 CTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCT 359

Qy        345 GGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAA 404
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 GGGGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAA 419

Qy        405 AAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGT 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 AAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGT 479

Qy        465 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 539

Qy        525 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 599

Qy        585 AGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 AGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 659

Qy        645 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 719

Qy        705 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 779
```

```
Qy        765 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 839

Qy        825 TGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCA 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 TGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCA 899

Qy        885 TTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAA 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 TTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAA 959

Qy        945 GTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGAT 1004
              |||||||||||||||| |||||||||| ||||||||||||||||||:||   |||
Db        960 GTTTATGTATACATCTTAATGAAAAGC-AAGCTAAATATGTTTACAGACMAA---GTGTG 1015

Qy       1005 TTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATA 1064
                |  : :  ||||:|||||||||| |  ||  :   |  |||||||||  ||
Db       1016 ATTYMCMCTGTTTTWAATCTAGCATATTCATTTGCTY----AATCAAAGTGGTTCATATT 1071

Qy       1065 TTTTTTTTAGTTGGTTA 1081
              |||||  | | | | ||
Db       1072 TTTTTAGTKGGTAGATA 1088


RESULT 6
BX387691
LOCUS       BX387691               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI037YD19 5-PRIME, mRNA sequence.
ACCESSION   BX387691
VERSION     BX387691.1  GI:30461701
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AI037CB10QP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AI037CB10QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI037YD19"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      286 a    257 c    274 g    306 t     78 others
ORIGIN

  Query Match            68.5%;  Score 861.6;  DB 13;  Length 1201;
  Best Local Similarity  95.7%;  Pred. No. 2.4e-133;
  Matches  915;  Conservative   10;  Mismatches   26;  Indels    5;  Gaps    4;

Qy         45 CGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGC 104
              |||  |||||||||||||| |   |||||||||||||||||||||||||||||||||||
Db         57 CGGGATCGGAGCGCGGCGGA-CAGNACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGC 115

Qy        105 CTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCC 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 CTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCC 175

Qy        165 CCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGC 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGC 235

Qy        225 GCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGAC 284
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        236 GCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG-TCCGGCAGAGGGAGGTGGTGGAC 294

Qy        285 CTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        295 CTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCYCT 354

Qy        345 GGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAA 404
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        355 GGGGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAA 414

Qy        405 AAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGT 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGT 474

Qy        465 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACA 534

Qy        525 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 AAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGC 594

Qy        585 AGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 644
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        595 AGAAATGCATGCTGTNAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCT 654

Qy        645 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 CTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATT 714

Qy        705 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 AATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTG 774

Qy        765 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 GATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGA 834

Qy        825 TGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCA 884
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        835 TGGAATWCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTYCA 894

Qy        885 TTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAA 944
              ||||||||||||||||||||||||:||||||||| :|||||||||||||||||||:
Db        895 TTTGCTACCTCTTTTTTTATTATGCCTYGGAATGGTT-MCTTAAATGACATTTTAAATAW 953

Qy        945 GTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTG 1000
              || ||||||||      | |||||    || :|:||||||||:     | |: |||
Db        954 GTGTATGTATAATCTGTATTGAAA--GCAAYSTMAATATGTTWCAGACCAARTGTG 1007


RESULT 7
BX387690/c
LOCUS       BX387690               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX387690 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI037YD19 3-PRIME, mRNA sequence.
ACCESSION   BX387690
VERSION     BX387690.1  GI:30461700
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AI037CB10NP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AI037CB10NP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI037YD19"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      358 a    232 c    212 g    308 t     91 others
ORIGIN

  Query Match             67.0%;  Score 842.6;  DB 13;  Length 1201;
  Best Local Similarity   85.6%;  Pred. No. 3.5e-130;
  Matches  946;  Conservative   22;  Mismatches  129;  Indels    8;  Gaps    4;

Qy        146 CCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCA 205
              :| :| :|| :      ||  : | |    || : ||||| |  || :  ||  ||
Db       1097 YCGVGTSCCRKAKCGGACCATSTACCCAGGCCCSCGCCTCCCGTAGCGSTCGCGCCTCTG 1038

Qy        206 GCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCG 265
              |    :   |   |||  || :| :| :  |:          |||    ||| | |
Db       1037 CGCTCWGCTSTGCRCAGCCGCGCCTYRGCBCTYTKAKATCCCARGGAAGCAAAAGCGCAG 978

Qy        266 GCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC 325
               | :   |||| | |:|     |   |  | |||||||    ||||||||||:|||||||
Db        977 CCCSGCAGAGGAGTTSGTGACCTKATAATGGATGTGCT--ACAGGGCCAGCAKGAGTGCC 920

Qy        326 TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCG 385
              ||     ||   |   ||  |||| ||||  |||||||:     |  ||||||||||||
Db        919 TG---TCGATACGGAGCCCTGGGCAAATGGCATTCCGGK--ACACCTGGATCCCAGGTCG 865

Qy        386 GGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGAC 445
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        864 GGAT-GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGTAC 806

Qy        446 ACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAAT 505
              ||||:|||||||||||||||||||||||||||||||||||||||:||||||||:|:|
Db        805 ACCCWACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGMTCTTGGGAMAWT 746

Qy        506 TGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 565
              |||||||||||||| ||| |||||||||||| |||| |||||||| | |||||
Db        745 TGCGGAGTGTACATTCACACAGATGCGTTCAAATAGNGCTCTNAGAGTTTTGNTNAGTGG 686

Qy        566 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 625
              |||||||||||||||| ||||||| ||| ||||||||||||||| | ||||||||||||
Db        685 CTCACTTCGGCTAAAANGCAGAAANGCANGCTGTCAGCGTTGGTNTNTCACATTCAATGG 626

Qy        626 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCC 685
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        625 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTNATTTGGACCAAGGAAGCCC 566

Qy        686 TGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGG 745
              |||||||||||||||||||||||:|||| |||||||||||||||||||||||||||||
Db        565 TGAAATGAATTCAACAATTAATATWCATCGNACTTCTTCTGTGGAAGGACTTTGTGAAGG 506

Qy        746 AATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAA 805
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||| ||
Db        505 AATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGNACTTGTTCAGATTACCCAAA 446

Qy        806 AGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA 865
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||| ||||||||
Db        445 AGGAGATGCTTCTACTGGATGGAATTCAGTCTCTCGCATCATTATTGAAGNACTACCAAA 386

Qy        866 ATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACT 925
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 ATNAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACT 326

Qy        926 TAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGT 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGT 266

Qy        986 TTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCA 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCA 206

Qy       1046 ATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT 1105
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        205 ATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTNATAGTCACATT 146

Qy       1106 CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCAT 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCAT 86

Qy       1166 TTTTAAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTT 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db          85 TTTTAAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAANAATTTTTT 26

Qy       1226 TTATATCTGTTAAATAAAAATTATT 1250
              ||||||||||:|  |||| || ||
Db          25 TTATATCTGTTWATAAAAATTTTTT 1


RESULT 8
BM560093
LOCUS       BM560093               1132 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6592628 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5476455
            5', mRNA sequence.
ACCESSION   BM560093
VERSION     BM560093.1  GI:18804229
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1132)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1992  row: o  column: 16
            High quality sequence stop: 638.
FEATURES              Location/Qualifiers
     source           1. .1132
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5476455"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      278 a    260 c    297 g    297 t
ORIGIN

  Query Match             67.0%;  Score 842.2;  DB 12;  Length 1132;
  Best Local Similarity   96.1%;  Pred. No. 4.1e-130;
  Matches  895;  Conservative    0;  Mismatches   33;  Indels    3;  Gaps    3;

Qy         52 GGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGC 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGC 60

Qy        112 TCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGC 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGC 120

Qy        172 GGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTG 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTG 180

Qy        232 AGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATA 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATA 240

Qy        292 ATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCA 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCA 300

Qy        352 ATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGG 411
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGG 360

Qy        412 AATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGA 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGA 420

Qy        472 GTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGC 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGC 480

Qy        532 GTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATG 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATG 540

Qy        592 CATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCA 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCA 600

Qy        652 TTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTC 711
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        601 TTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAATGAATTCAACAATTAATATTC 660

Qy        712 ATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTG 771
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        661 ATCGCACTTCTTCTGTGGGAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTG 720

Qy        772 CTATCTGGG-TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAAT 830
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTATCTGGGTTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAAT 780

Qy        831 TCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCT 890
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        781 TCAGTTTCTCGCATCATTATTGAAAGACTACCCAAATAAATGCTTTAATTTTCATTTGCT 840

Qy        891 ACCT-CTTTTTTTATTATGCCTTGGAAT-GGTTCACTTAAATGACATTTTAAATAAGTTT 948
              ||||  |||||||||  ||  ||||||||||  ||||||||||| |||  |||||||||| ||
Db        841 ACCTCCTTTTTTTAATAGGCCTTGGAATGGGTTCACTTAAAGGACTTTTTAAATAAGGTT 900

Qy        949 ATGTATACATCTGAATGAAAAGCAAAGCTAA 979
                  | | ||      |  |  || || ||
Db        901 TATGGAATACCTCCGGAATGAAAAAGGCAAA 931


RESULT 9
BI763295
LOCUS       BI763295                903 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603047656F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188069 5',
            mRNA sequence.
ACCESSION   BI763295
VERSION     BI763295.1  GI:15754873
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11469  row: o  column: 14
            High quality sequence stop: 875.
FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5188069"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      274 a    137 c    178 g    313 t      1 others
ORIGIN

  Query Match             64.9%;  Score 815.2;  DB 12;  Length 903;
  Best Local Similarity   96.4%;  Pred. No. 1.3e-125;
  Matches  855;  Conservative    0;  Mismatches   29;  Indels    3;  Gaps    2;

Qy        362 GGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAG 421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          1 GGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGGG 60

Qy        422 GGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAA 120
```

```
Qy        482 TTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAG 180

Qy        542 TGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCA 601
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        181 TGCTCTAAGAGTTTTGTTCAGGGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCA 240

Qy        602 GCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTAT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTAT 300

Qy        662 AATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTC 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTC 360

Qy        722 TTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGT 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGT 420

Qy        782 TGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCG 841
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCG 480

Qy        842 CATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTT 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTT 540

Qy        902 TATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTG 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTG 600

Qy        962 AATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAA 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAA 660

Qy       1022 TCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATA-TTTTTTTTAGTTGGTT 1080
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        661 TCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTTAGTTGGTT 720

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              |||||||||||||||||||||||||||||| |||||||||||||||||  || |||||
Db        721 AGAATACTTTCTTCATAGTCACATTCTCTCAANCTATAATTTGGAATATTCGTGGGGTCT 780

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              || |  || |||||||||||||||||||||||||| ||||||||||||||||| ||||
Db        781 TTAG--TTATCTCTTAGTATAGCATTTTTAAAAAAATTTAAAAGCTACCAATCTTCGTAC 838

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATT 1247
              |||||||||   | |  | |||||| ||| | |    || |  | ||
Db        839 AATTTGTAATGTTAAGAATTTTTTTATATCTGTTAATAAAATTATTT 885
```

```
RESULT 10
AL544722
LOCUS       AL544722                887 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL544722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI022YF04 5-PRIME, mRNA sequence.
ACCESSION   AL544722
VERSION     AL544722.2  GI:31266563
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12877202.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4941.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI022DC02QP1&cluster=4941.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI022DC02QP1.
FEATURES              Location/Qualifiers
     source           1. .887
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI022YF04"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      215 a    211 c    241 g    220 t
ORIGIN
```

```
  Query Match             64.5%;  Score 811.2;  DB 9;  Length 887;
  Best Local Similarity   99.5%;  Pred. No. 5.9e-125;
  Matches  824;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         69 GACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAG 128
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAG 120

Qy        129 CCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTG 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTG 180

Qy        189 CTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG 240

Qy        249 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAA 308
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAAAGGCGCAG-TCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAA 299

Qy        309 GGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACA 368
              |||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        300 GGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTACA 359

Qy        369 CCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGC 428
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGC 419

Qy        429 TTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGC 488
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGC 479

Qy        489 ATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTA 548
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTA 539

Qy        549 AGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGG 608
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGG 599

Qy        609 TATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTAT 668
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 TATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTAT 659

Qy        669 TTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTG 728
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 TTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTG 719

Qy        729 GAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACT 788
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACT 779

Qy        789 TGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATT 848
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 TGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATT 839

Qy        849 ATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCT 896
                |||||||||||||||||||||||||||||||||||||||||||||||
Db        840 ATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCT 887


RESULT 11
BQ425266
LOCUS       BQ425266                851 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7912803 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150166
            5', mRNA sequence.
ACCESSION   BQ425266
VERSION     BQ425266.1  GI:21120581
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13484  row: f  column: 23
            High quality sequence stop: 670.
FEATURES             Location/Qualifiers
     source          1. .851
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6150166"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      186 a    224 c    258 g    183 t
ORIGIN

  Query Match           58.8%;  Score 739.4;  DB 13;  Length 851;
  Best Local Similarity   99.1%;  Pred. No. 5e-113;
  Matches  754;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          6 GAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 GAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG 95

Qy         66 CCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 CCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGG 155

Qy        126 CAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTC 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTC 215

Qy        186 CTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGG 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGG 275

Qy        246 AAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 AAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTA 335

Qy        306 CAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGT 365
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        336 CAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGT 395

Qy        366 ACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAA 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAA 455

Qy        426 AGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTAT 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 AGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTAT 515

Qy        486 GGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCT 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCT 575

Qy        546 CTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGT 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGT 635

Qy        606 TGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATT 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATT 695

Qy        666 TATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCT 725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 TATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCT 755

Qy        726 GTGGAAGGACTTTGTG-AAGGAATTGGTGCTGGATTAGTGG 765
              ||||||||||||||||| |||||||||||||||||| |  | |
Db        756 GTGGAAGGACTTTGTGAAAGGAATTGGTGCTGGAATTATTG 796


RESULT 12
BQ425098
LOCUS       BQ425098                922 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7902947 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157844
            5', mRNA sequence.
ACCESSION   BQ425098
VERSION     BQ425098.1  GI:21120413
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13504  row: f  column: 21
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1. .922
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6157844"
                     /tissue_type="melanotic melanoma"
```

```
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      209 a    236 c    252 g    224 t      1 others
ORIGIN

  Query Match           57.0%;  Score 716.4;  DB 13;  Length 922;
  Best Local Similarity   89.4%;  Pred. No. 3.3e-109;
  Matches  816;  Conservative    0;  Mismatches   92;  Indels    5;  Gaps    4;

Qy         25 CGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTC 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 CGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCCAGACGCTGACCACGTTC 69

Qy         85 CTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGAC 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCCATGCGAC 129

Qy        145 CCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGC 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGC 189

Qy        205 AGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAGCTCC 249

Qy        265 GGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGC 309

Qy        325 CTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTC 384
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        310 CTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGATCCCAGGTC 369

Qy        385 GGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGA 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 GGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGA 429

Qy        445 CACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA 489

Qy        505 TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTG 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTG 549

Qy        565 GCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATG 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATG 609

Qy        625 GAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCC 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCC 669

Qy        685 CTGAAATGAATTCAACAATTAATATTCATCGCACTT-CTTCTGTGGAAGGACTTTGTG-A 742
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db        670 CTGAAATGAATTCAACAATTAATATTCATCGCACTTCCTTCTGTGGAAGGACTTTGTGAA 729

Qy        743 AGGAATTGGTGCT-GGATTAGTGGATGTTGC--TATCTGGGTTGGCACTTGTTCAGATTA 799
              |||||||||||||| |||||| ||||||||||       ||||||||||||||   | |
Db        730 AGGAATTGGTGCTGGGATTANTGGATGTTGCCTATCTGGGGTTGGCACTTGTTTCCAATT 789

Qy        800 CCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACT 859
               ||  || | ||       | ||   ||| |   |  |||  |  |  |
Db        790 ACCCCAAAGGGAGATGCTTTCTTACTGGGAGGGAAATTCCAGTTTTCTCGCCATCATTTA 849

Qy        860 ACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGG 919
              .    || || | |    || |   ||  |       |||||  |||  ||||
Db        850 TTTGGAAGAACTACCCAAAATAAAATGCGTCTTAAATTTTTCCATTTGGCCTACCCCCCT 909

Qy        920 TTCACTTAAATGA 932
              |||  | |||| |
Db        910 TTCTTTGAAATTA 922


RESULT 13
BM915926
LOCUS       BM915926                1037 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6639781 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482196
            5', mRNA sequence.
ACCESSION   BM915926
VERSION     BM915926.1  GI:19366305
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2007  row: n  column: 21
            High quality sequence stop: 482.
FEATURES             Location/Qualifiers
     source          1. .1037
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5482196"
                     /tissue_type="amelanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_41"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      218 a    310 c    291 g    218 t
ORIGIN

  Query Match           56.1%;  Score 705.4;  DB 12;  Length 1037;
  Best Local Similarity   91.7%;  Pred. No. 2.2e-107;
  Matches  791;  Conservative    0;  Mismatches   66;  Indels    6;  Gaps    4;

Qy         53 GAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCT 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCGCGGCGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCT 60

Qy        113 CCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCG 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCGCTGCCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCG 120

Qy        173 GCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGA 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGA 180

Qy        233 GATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAA 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATCCCCAAGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAA 240

Qy        293 TGGAATGTGCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAA 352
```

```
Db        241 TGGAATGTGCTTACCAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAA 300

Qy        353 TGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGA 412

Db        301 TGGCATTCCGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGA 360

Qy        413 ATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAG 472

Db        361 ATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAG 420

Qy        473 TTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCG 532

Db        421 TTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCG 480

Qy        533 TTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGC 592

Db        481 TTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCACAAATGC 540

Qy        593 ATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCAT 652

Db        541 ATGCTGTCAGCGTTGGTATTTCACGTTCAATGGAGCTGAATGTTCAGGACCTCTTCCCAT 600

Qy        653 TGAAGCTATAATTTATTTGGACCAAGGAAGCCCT-GAAATGAATTCAACAATTAATATTC 711

Db        601 TGAAGCTATAATTTATTTGGACCAACGAAGCCCTGGAAATGAATTCCACAATTAGTATTC 660

Qy        712 ATC-GCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTT 770

Db        661 ATCGGCACTTCTTCTGTGGAAAGACTTTGCGAAGGAATTGGTGCTGGATTAGTGGATGTT 720

Qy        771 GCTATCTGGGTT--GGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTAC--TGGATG 826

Db        721 GCTATCGGGGTTGGGGACTTTGTTCACATTACCCCAAAGGAAATGCTTCCACCTGGCCGG 780

Qy        827 GAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATT 886

Db        781 AATGTCCGCCTGTCCCTCTCCGAGTGGACGAATCCCCAAACTCACGCCTTTAACTTGACT 840

Qy        887 TGCTACCTCTTTTTTTATTATGC 909

Db        841 TGGGCAGACTCCTCTTCGGAAGC 863


RESULT 14
CA415410/c
LOCUS       CA415410                747 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-EZ0-baw-n-12-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone
            UI-H-EZ0-baw-n-12-0-UI 3', mRNA sequence.
ACCESSION   CA415410
VERSION     CA415410.1  GI:24778061
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-60, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .747
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-H-EZ0-baw-n-12-0-UI"
                      /tissue_type="Chondrosarcoma Grade II"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="NCI_CGAP_Ch1"
                      /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                      with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      NCI_CGAP_Ch1 is a cDNA library containing the following
                      tissue(s): Chondrosarcoma Grade II. The library was
                      constructed according to Bonaldo, Lennon and Soares,
                      Genome Research, 6:791-806, 1996. First strand cDNA
                      synthesis was primed with an oligo-dT primer containing a
                      Not I site. Double stranded cDNA was ligated to an EcoR I
                      adaptor, digested with Not I, and cloned directionally
                      into pT7T3-Pac vector. The oligonucleotide used to prime
                      the synthesis of first-strand cDNA contains a library tag
                      sequence that is located between the Not I site and the
                      (dT)18 tail. The sequence tag for this library is
                      TGATCACGCT.
                      TAG_LIB=UI-H-EZ0
                      TAG_TISSUE=grade-2-chondrosarcoma
                      TAG_SEQ=ATCTAATATG"
BASE COUNT      277 a    121 c    113 g    236 t
ORIGIN

  Query Match             55.7%;  Score 700.4;  DB 14;  Length 747;
  Best Local Similarity   98.9%;  Pred. No. 1.5e-106;
  Matches  716;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    1;

Qy        534 TCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCA 593

Db        742 TCAAATAGTGCTCTAAGAGTTT--GTTCAGTGCTCACTTCGGCTAAAATGCAGAAATGCA 685

Qy        594 TGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATT 653

Db        684 TGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATT 625

Qy        654 GAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCAT 713

Db        624 GAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCAT 565

Qy        714 CGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCT 773

Db        564 CGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCT 505

Qy        774 ATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCA 833

Db        504 ATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCA 445

Qy        834 GTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACC 893

Db        444 GTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACC 385

Qy        894 TCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTA 953

Db        384 TCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTA 325

Qy        954 TACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTG 1013

Db        324 TACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTG 265

Qy       1014 TTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTA 1073

Db        264 TTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTA 205

Qy       1074 GTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTT 1133
```

```
Db        204 GTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTT 145

Qy       1134 GTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATC 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATC 85

Qy       1194 TTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCC 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          84 TTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCC 25

Qy       1254 AACA 1257
              ||||
Db          24 AACA 21


RESULT 15
BQ008675/c
LOCUS       BQ008675                796 bp    mRNA    linear   EST 26-MAR-2002
DEFINITION  UI-H-EI0-ayl-c-24-0-UI.s1 NCI_CGAP_EI0 Homo sapiens cDNA clone
            IMAGE:5840207 3', mRNA sequence.
ACCESSION   BQ008675
VERSION     BQ008675.1  GI:19733576
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            The following repetitive elements were found in this cDNA
            sequence: 24-57, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .796
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5840207"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_EI0"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_EI0 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is ACACTTGCAC.
                     TAG_LIB=UI-H-EI0
                     TAG_TISSUE=chondrosarcoma
                     TAG_SEQ=ACACTTGCAC"
BASE COUNT      292 a    132 c    120 g    252 t
ORIGIN
```

```
  Query Match           55.3%;  Score 695.6;  DB 12;  Length 796;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-106;
  Matches  693;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 GCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATG 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 GCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATG 651

Qy        625 GAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCC 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 GAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCC 591

Qy        685 CTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 CTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG 531

Qy        745 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAA 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAA 471

Qy        805 AAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAA 864
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 AAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAA 411

Qy        865 AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCAC 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCAC 351

Qy        925 TTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATG 984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATG 291

Qy        985 TTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTC 1044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 TTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTC 231

Qy       1045 AATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACAT 1104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 AATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACAT 171

Qy       1105 TCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCA 1164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCA 111

Qy       1165 TTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTT 1224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTT 51

Qy       1225 TTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||
Db         50 TTTATATCTGTTAAATAAAAATTATTTCCAACA 18


Search completed: August 20, 2003, 14:44:10
Job time : 2975 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 12:35:55 ; Search time 89 Seconds
(without alignments)
6233.917 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1231.6	98.0	1342	4	US-09-489-847-89	Sequence 89, Appl
	2	1222.8	97.3	1286	4	US-09-489-847-124	Sequence 124, App
	3	1197	95.2	1288	4	US-09-205-258-125	Sequence 125, App
c	4	681.8	54.2	683	4	US-09-222-575-63	Sequence 63, Appl
c	5	681.8	54.2	683	4	US-09-389-681-63	Sequence 63, Appl
c	6	681.8	54.2	683	4	US-09-620-405B-63	Sequence 63, Appl
c	7	681.8	54.2	683	4	US-09-339-338-63	Sequence 63, Appl
c	8	681.8	54.2	683	4	US-09-433-826B-63	Sequence 63, Appl
c	9	681.8	54.2	683	4	US-09-604-287A-63	Sequence 63, Appl
	10	56.8	4.5	20674	4	US-09-641-638-651	Sequence 651, App
c	11	55.2	4.4	2109	4	US-09-370-838-153	Sequence 153, App
	12	55	4.4	4818	3	US-08-817-926-27	Sequence 27, Appl
c	13	54.2	4.3	19124	2	US-08-487-826B-13	Sequence 13, Appl
	14	52.8	4.2	7244	3	US-08-378-313-26	Sequence 26, Appl
c	15	52	4.1	6243	2	US-09-056-075-1	Sequence 1, Appli
c	16	50.4	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
	17	48.8	3.9	53332	4	US-09-801-861-3	Sequence 3, Appli
c	18	48.6	3.9	1866	3	US-08-909-742-1	Sequence 1, Appli
c	19	48.6	3.9	1866	3	US-09-412-289-1	Sequence 1, Appli
	20	47.6	3.8	4383	4	US-08-397-653B-2	Sequence 2, Appli
	21	47.6	3.8	4383	6	5175095-4	Patent No.5175095
c	22	47.6	3.8	5852	1	US-07-867-106-2	Sequence 2, Appli
c	23	47.2	3.8	3095	6	5231168-1	Patent No. 5231168
c	24	46.2	3.7	10640	4	US-09-417-485D-5	Sequence 5, Appli
c	25	46	3.7	4060	1	US-08-308-949A-1	Sequence 1, Appli
	26	45.8	3.6	1785	4	US-09-601-198-156	Sequence 156, App
	27	45.6	3.6	636	3	US-08-998-416-1137	Sequence 1137, Ap
	28	45.6	3.6	837	3	US-08-998-416-288	Sequence 288, App
c	29	45.6	3.6	6124	4	US-08-213-419B-3	Sequence 3, Appli
	30	45.4	3.6	1098	4	US-09-252-991A-14024	Sequence 14024, A
c	31	45.4	3.6	1335	4	US-09-252-991A-7551	Sequence 7551, Ap
c	32	45.4	3.6	1401	4	US-09-252-991A-7622	Sequence 7622, Ap
	33	45.4	3.6	1611	4	US-09-252-991A-7930	Sequence 7930, Ap
	34	45.2	3.6	680	3	US-08-998-416-204	Sequence 204, App
	35	45.2	3.6	2450	4	US-09-491-522-9	Sequence 9, Appli
c	36	45.2	3.6	3909	4	US-09-016-434-1119	Sequence 1119, Ap
	37	45.2	3.6	4580	4	US-09-491-522-8	Sequence 8, Appli
c	38	45	3.6	390	3	US-08-911-853-20	Sequence 20, Appl
c	39	45	3.6	390	3	US-09-479-409-20	Sequence 20, Appl
c	40	45	3.6	390	4	US-09-479-453-20	Sequence 20, Appl
	41	45	3.6	3103	3	US-08-826-246-3	Sequence 3, Appli
	42	45	3.6	3103	3	US-08-944-495-3	Sequence 3, Appli
	43	45	3.6	3103	3	US-09-126-640-2	Sequence 2, Appli
	44	45	3.6	3103	3	US-08-925-588-3	Sequence 3, Appli
	45	45	3.6	3103	4	US-09-288-292A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-489-847-89
; Sequence 89, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-89

Query Match 98.0%; Score 1231.6; DB 4; Length 1342;
Best Local Similarity 99.6%; Pred. No. 2.4e-273;
Matches 1245; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```
Qy          8 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCC 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         12 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG-C 70

Qy         68 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 130

Qy        128 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 190

Qy        188 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 250
```

```
Qy       248 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       251 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 310

Qy       308 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTAC 367
            |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       311 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTAC 370

Qy       368 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 427
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       371 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 430

Qy       428 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 487
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       431 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 490

Qy       488 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 547
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       491 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 550

Qy       548 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 607
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       551 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTG 610

Qy       608 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 667
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       611 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 670

Qy       668 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 727
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       671 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 730

Qy       728 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 787
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       731 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 790

Qy       788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       791 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 850

Qy       848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       851 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 910

Qy       908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       911 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 970

Qy       968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1027
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       971 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1030

Qy      1028 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1087
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1031 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1090

Qy      1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1091 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1150

Qy      1148 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1207
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1151 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1210

Qy      1208 AAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
            |||||||||||||||||||||||||||||||||||||||||||||||| |
Db      1211 AAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAAAA 1260
```

RESULT 2
US-09-489-847-124
; Sequence 124, Application US/09489847
; Patent No. 6476195

```
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
;   LENGTH: 1286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1284)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-124
```

Query Match 97.3%; Score 1222.8; DB 4; Length 1286;
Best Local Similarity 99.7%; Pred. No. 2.4e-271;
Matches 1246; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```
Qy         8 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCC 67
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         2 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG-C 60

Qy        68 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 120

Qy       128 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 180

Qy       188 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 240

Qy       248 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 307
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GCAAAAGGCGCA-CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 299

Qy       308 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTAC 367
             |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       300 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTAC 359

Qy       368 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       360 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 419

Qy       428 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       420 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 479

Qy       488 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       480 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 539

Qy       548 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 607
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       540 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 599
```

```
Qy        608 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 659

Qy        668 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 719

Qy        728 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 779

Qy        788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 839

Qy        848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 899

Qy        908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 959

Qy        968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1019

Qy       1028 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1079

Qy       1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1139

Qy       1148 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1199

Qy       1208 AAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 AAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1249
```

RESULT 3
US-09-205-258-125
; Sequence 125, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1286)
; OTHER INFORMATION: n equals a,t,g, or c

```
US-09-205-258-125

  Query Match             95.2%;  Score 1197;  DB 4;  Length 1288;
  Best Local Similarity   99.3%;  Pred. No. 2e-265;
  Matches 1242;  Conservative    2;  Mismatches    2;  Indels    5;  Gaps    4;

Qy          8 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAGCC 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :|
Db          1 GGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGA-SC 59

Qy         68 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCA 119

Qy        128 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCCT 179

Qy        188 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAA 239

Qy        248 GCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 307
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCAAAAGGCGCA--TCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACA 297

Qy        308 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTAC 367
              |||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Db        298 AGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTAC 357

Qy        368 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAG 417

Qy        428 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 CTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGG 477

Qy        488 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 CATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCT 537

Qy        548 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTG 597

Qy        608 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTA 657

Qy        668 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGT 717

Qy        728 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCAC 777

Qy        788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 837

Qy        848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 897

Qy        908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 957

Qy        968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1027
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        958 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACA-TGTTTTTAAATCTAGC 1016

Qy       1028 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTTAGAATAC 1087
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTAGTTGGTTAGAATAC 1076

Qy       1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTT-GGAATATTGTTGTGGTCTTTTGTT 1146
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1077 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTT 1136

Qy       1147 TTTTCTCTTAGTATAGCATTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 TTTTCTCTTAGTATAGCATTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTG 1196

Qy       1207 TAAATGTTAAGAATTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              |||||||||||||||||||||||||||||||||||||||||||||||:|||
Db       1197 TAAATGTTAAGAATTTTTTTATATCTGTTAAATAAAAATTATTTCCMACA 1247

RESULT 4
US-09-222-575-63/c
; Sequence 63, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
;  APPLICANT: Yuqiu, Jiang
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 210121.470
;  CURRENT APPLICATION NUMBER: US/09/222,575
;  CURRENT FILING DATE:  1998-12-28
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 683
;   TYPE: DNA
;   ORGANISM: Human
US-09-222-575-63

  Query Match             54.2%;  Score 681.8;  DB 4;  Length 683;
  Best Local Similarity   99.6%;  Pred. No. 2.5e-147;
  Matches  680;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTAAATCTAGCATTATTCATTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTAAATCTAGCATTATTCATTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 5
US-09-389-681-63/c
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 683
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-389-681-63

```
  Query Match             54.2%;  Score 681.8;  DB 4;  Length 683;
  Best Local Similarity   99.6%;  Pred. No. 2.5e-147;
  Matches  680;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTATTATGCCTTGGAATGGTCACTTAAATGACAT 935
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTATTATGCCTTGGAATGGTCACTTAAATGACAT 264
```

```
Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTAAATCTAGCATTATTCATTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTAAATCTAGCATTATTCATTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 6
US-09-620-405B-63/c
; Sequence 63, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 683
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-620-405B-63

```
  Query Match             54.2%;  Score 681.8;  DB 4;  Length 683;
  Best Local Similarity   99.6%;  Pred. No. 2.5e-147;
  Matches  680;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324
```

```
Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 7
US-09-339-338-63/c
; Sequence 63, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 2.5e-147;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 8
US-09-433-826B-63/c
; Sequence 63, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 2.5e-147;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
```

```
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 9
US-09-604-287A-63/c
; Sequence 63, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;
Best Local Similarity 99.6%; Pred. No. 2.5e-147;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy        516 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGG 624

Qy        576 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 CTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGT 564

Qy        636 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAAT 504

Qy        696 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCT 444

Qy        756 GGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCT 815
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        443 GGATTAGTGGATGTTGCTATCTGGGTTGGYACTTGTTCAGATTACCCAAAAGGAGATGCT 384

Qy        816 TCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTT 875
              ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db        383 TCTACTGGATGGAATTCAGTTTCTCGYATCATTATTGAAGAACTACCAAAATAAATGCTT 324

Qy        876 TAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 935
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        323 TAATTTTCATTTGCTACCWCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACAT 264

Qy        936 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCA 204

Qy        996 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTG 144

Qy       1056 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCT 84

Qy       1116 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAA 24

Qy       1176 ATATAAAAGCTACCAATCTTTGT 1198
              |||||||||||||||||||||||
Db         23 ATATAAAAGCTACCAATCTTTGT 1
```

RESULT 10
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1123..3123
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 3124..3297
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 3871..4072
; OTHER INFORMATION: exon 2

; NAME/KEY: exon
; LOCATION: 5552..5633
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 5758..5880
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: 5996..6099
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: 6349..6509
; OTHER INFORMATION: exon 6
; NAME/KEY: exon
; LOCATION: 7379..7522
; OTHER INFORMATION: exon 7
; NAME/KEY: exon
; LOCATION: 8645..8854
; OTHER INFORMATION: exon 8
; NAME/KEY: exon
; LOCATION: 12254..12340
; OTHER INFORMATION: exon 9
; NAME/KEY: exon
; LOCATION: 12854..13023
; OTHER INFORMATION: exon 10
; NAME/KEY: exon
; LOCATION: 13308..13429
; OTHER INFORMATION: exon 11
; NAME/KEY: exon
; LOCATION: 16567..16667
; OTHER INFORMATION: exon 12
; NAME/KEY: exon
; LOCATION: 16775..16945
; OTHER INFORMATION: exon 13
; NAME/KEY: exon
; LOCATION: 17063..17554
; OTHER INFORMATION: exon 14
; NAME/KEY: misc_feature
; LOCATION: 17555..20674
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1128
; OTHER INFORMATION: 10-508-191 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1182
; OTHER INFORMATION: 10-508-245 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1559
; OTHER INFORMATION: 10-509-284 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 1570
; OTHER INFORMATION: 10-509-295 : deletion of C
; NAME/KEY: allele
; LOCATION: 1827
; OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
; NAME/KEY: allele
; LOCATION: 2048
; OTHER INFORMATION: 10-511-62 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2323
; OTHER INFORMATION: 10-511-337 : insertion of T
; NAME/KEY: allele
; LOCATION: 2341
; OTHER INFORMATION: 10-512-36 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 2623
; OTHER INFORMATION: 10-512-318 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2832
; OTHER INFORMATION: 10-513-250 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2844
; OTHER INFORMATION: 10-513-262 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2934
; OTHER INFORMATION: 10-513-352 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2947
; OTHER INFORMATION: 10-513-365 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 3802
; OTHER INFORMATION: 12-206-81 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 4062
; OTHER INFORMATION: 10-343-231 : deletion of C
; NAME/KEY: allele
; LOCATION: 4088
; OTHER INFORMATION: 12-206-366 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4109
; OTHER INFORMATION: 10-343-278 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4170
; OTHER INFORMATION: 10-343-339 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 5903
; OTHER INFORMATION: 10-346-23 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6019
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6141
; OTHER INFORMATION: 10-346-263 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6183
; OTHER INFORMATION: 10-346-305 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 6338
; OTHER INFORMATION: 10-347-74 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6375
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6429
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 6467
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6484
; OTHER INFORMATION: 10-347-220 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6534
; OTHER INFORMATION: 10-347-271 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 6611
; OTHER INFORMATION: 10-347-348 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 7668
; OTHER INFORMATION: 10-348-391 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 8608
; OTHER INFORMATION: 10-349-47 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 8658
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 8703
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 8777
; OTHER INFORMATION: 10-349-216 : deletion of CTG
; NAME/KEY: allele
; LOCATION: 8785
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 8926

```
;   OTHER INFORMATION: 10-349-368  : polymorphic base C or T
;   NAME/KEY: allele
;   LOCATION: 12171
;   OTHER INFORMATION: 10-350-72  : polymorphic base C or T
;   NAME/KEY: allele
;   LOCATION: 12429
;   OTHER INFORMATION: 10-350-332  : polymorphic base C or T
;   NAME/KEY: allele
;   LOCATION: 13341
;   OTHER INFORMATION: 10-507-170  : polymorphic base A or G
;   NAME/KEY: allele
;   LOCATION: 13492
;   OTHER INFORMATION: 10-507-321  : polymorphic base A or C
;   NAME/KEY: allele
;   LOCATION: 13524
;   OTHER INFORMATION: 10-507-353  : polymorphic base C or T
;   NAME/KEY: allele
;   LOCATION: 13535

  Query Match             4.5%;  Score 56.8;  DB 4;  Length 20674;
  Best Local Similarity   46.3%;  Pred. No. 0.0026;
  Matches  187;  Conservative    0;  Mismatches  217;  Indels    0;  Gaps    0;

Qy        845 CATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTAT 904
              | || || || | |||   |||  | |    || |||| ||||  ||  | ||  ||||
Db      11062 CTTTTTTTAATAGCTAAGGAAAATATTTTAATATTTTTAATTTAATAAATTTTAATTTAA 11121

Qy        905 TATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAAT 964
              |||       ||   || | || |||   |  |||||    |   | || | | | | |
Db      11122 TATTAAAATTAAAATTTAATTTAATATTAAATTAAAATTTTAATTTAAATAAATAATT 11181

Qy        965 GAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCT 1024
               |||   |||   |  ||  |||| |    ||| |    ||| |       |||||||
Db      11182 AAAATTTAAATAAATTTAAATTTAAAATTTAAATTTAATTTTAAATAAACATTTAAATTT 11241

Qy       1025 AGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAA 1084
              |||  |    ||   || | | ||       || | |    ||  |      | | |
Db      11242 TTAATTTTAATATTAAATTAATTTAATTTAATATTAATTTAACTTAATTTAATTTAATAT 11301

Qy       1085 TACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTG 1144
              || |||      | | |  |  | | |   || | |      || | || |    |||
Db      11302 TAATTTAACTTAATTTAATTAATTTAATATTAAATTAAATTTTAATATTTTTAATTTTAA 11361

Qy       1145 TTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATT 1204
              | ||   |     ||    | ||| | |  |||  |     |   ||| ||  |    |
Db      11362 TATTAATTTAATTTAATTTAATTTAATATTAATTAATTTAATTTTAATTTTAATTGCTTC 11421

Qy       1205 TGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTA 1248
                ||     | | | |||  | | | | | ||||    ||||||
Db      11422 AATATTAAATTAAATTTTAATATTTTTATTTTAATATTAAATTA 11465


RESULT 11
US-09-370-838-153/c
; Sequence 153, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Mohamath, Roadoh
;  APPLICANT: Secrist, Heather
;  TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
;  TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.475C1
;  CURRENT APPLICATION NUMBER: US/09/370,838
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: US 09/285,323
;  EARLIER FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 153
;   LENGTH: 2109
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-370-838-153

  Query Match             4.4%;  Score 55.2;  DB 4;  Length 2109;
  Best Local Similarity   51.2%;  Pred. No. 0.0023;
  Matches  129;  Conservative    0;  Mismatches  123;  Indels    0;  Gaps    0;

Qy          6 GAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG 65
              || | || | || |     |||       | |    | |||||| ||  ||   ||   |
Db       1140 GACGGGCACCGGGGCTGCTCGCGCCCTCCCGGGGCCCCGCGGCCCCGCCGCCGCGCCCGG 1081

Qy         66 CCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGG 125
              |    |     || ||| |  |||||||  ||| ||| | |||  | | |     |||
Db       1080 CGCCGCCGCCTCCTCGTCCTCCTCCTCGTCCTCGTCCTCGTCCTCCCCGTCCTCCTCCGC 1021

Qy        126 CAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTC 185
              | |||  |   |   || |||   |||| | |||||  ||  |   |  |||||| ||||
Db       1020 CGGCCCCGGCGCTCCCGCCCCGCCGGCCTCCCCGCCAGCCGCCCCGGCGTCCGCGCCCTC 961

Qy        186 CTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGG 245
              |  | |   | || || |   | ||||  |   | | | |    ||||   |   || |
Db        960 CCACGGGGGCCGCCGCGGGCCCGGCCCCGGGAATGGCGTGAGCGTGAGCGGCGGCAGCGC 901

Qy        246 AAGCAAAAGGCG 257
               ||| | || ||
Db        900 CAGCGAGAGCCG 889


RESULT 12
US-08-817-926-27
; Sequence 27, Application US/08817926
; Patent No. 6001590
;  GENERAL INFORMATION:
;    APPLICANT:  Komeda, Toshihiro
;    APPLICANT:  Suda, Hisako
;    APPLICANT:  Tamai, Yukio
;    APPLICANT:  Iwamatsu, Akihiro
;    APPLICANT:  Kato, No. 6001590uo
;    APPLICANT:  Sakai, Yasuyoshi
;    TITLE OF INVENTION:  PROMOTER/TERMINATOR FOR CANDIDA BOIDINII
;    TITLE OF INVENTION:  FORMATE DEHYDROGENASE GENE
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,926
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP96/02597
;      FILING DATE:  12-SEP-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 234133/1995
;      FILING DATE:  12-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 42536/1996
;      FILING DATE:  29-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bent, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  081356/0112
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
```

```
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4818 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Candida boidinii
US-08-817-926-27

  Query Match             4.4%;  Score 55;  DB 3;  Length 4818;
  Best Local Similarity   45.5%;  Pred. No. 0.0036;
  Matches  196;  Conservative    0;  Mismatches  235;  Indels    0;  Gaps    0;

Qy        821 TGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATT 880
              | | || | |||| |   |       ||| | |     || ||||||  | | |   ||
Db       4077 TTGTTGAATTTCATTGATTATTTATATTTCTTAGATTTTAAAAAAATATTTTCCTCTTTT 4136

Qy        881 TTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAA 940
              || |||| |      ||||   |||     |   |       |    || | || |  |
Db       4137 TTTATTTTCCTTTGTTTTTCAAATTTAAAATGATAGAATGAAAGAATAAAAATATATATA 4196

Qy        941 ATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTG 1000
              ||   ||||   ||   |||     |     |||   || ||   ||| |    | | |
Db       4197 TTATTATTATTATTATTACTGTCAAACGTTTAAAAAGAAGTAGTATTAAACTTAACACTC 4256

Qy       1001 TGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTC 1060
              |  |      |   |  | | | |    |||    ||     ||   || ||| |  |||| 
Db       4257 TTCTGAGTTATAATGGTAATAACAGTGATTTAATATACCTTTTTTTTCCAAATTTTTTTC 4316

Qy       1061 AATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAAT 1120
              |||  ||  ||| | |  || |   | | |  | |      | |        ||  | |  |
Db       4317 AATTATTCATTTTGGTATTTGGTTAATTATGGTGAATAAAAAAAAAGAAAAATTTCTTGT 4376

Qy       1121 TTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATA 1180
              ||    | |||||      | || |  ||| | || ||||     ||| ||   | | |
Db       4377 TTCTTTTGTTGTTTATTCTTGTTTTAATTTTTTTTTGTATCAATCTTTAAATTTAGTTTT 4436

Qy       1181 AAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT 1240
              |||  |   | | ||  |  |||||  || | ||||   || |  ||| ||   | |
Db       4437 AAATTTTTTATTATTATTCTAATTTTAAATTATTAATTGTTGTAATTAAATTATTAATTA 4496

Qy       1241 AAAAATTATTT 1251
              |    | ||||
Db       4497 ATTTCTAATTT 4507


RESULT 13
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
;  GENERAL INFORMATION:
;    APPLICANT:  Sim, Kim L.
;    APPLICANT:  Chitnis, Chetan
;    APPLICANT:  Miller, Louis H.
;    APPLICANT:  Peterson, David S.
;    APPLICANT:  Su, Xin-zhaun
;    APPLICANT:  Wellems, Thomas E.
;    TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
;    TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe Martens Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,826B
;      FILING DATE:  10-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  NIH121.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19124 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-487-826B-13

  Query Match             4.3%;  Score 54.2;  DB 2;  Length 19124;
  Best Local Similarity   46.5%;  Pred. No. 0.0099;
  Matches  209;  Conservative    0;  Mismatches  238;  Indels    2;  Gaps    1;

Qy        788 TTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCAT 847
              || ||   |||     |||      |  || |  |  ||   ||| | ||| |   ||  |
Db      15954 TTTTTTTTATTTAATTAAATTTTTTTATTTTTTTTTTATTTCATTAAATTTTTTTAATTTT 15895

Qy        848 TATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTAT 907
              | || |   | |   |   |       | | |||||  |||  |   |    |||| ||||
Db      15894 TTTTTATTTAATTAAATTTTTTTATTTATTATTTTTTTTTTATTTAATTAAATTTTTTTAT 15835

Qy        908 GCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAA 967
              ||    |  || | ||||||  |  ||||   | | ||||||||||| || |   |
Db      15834 TTATTATTTTTTTTTTATTTAAATAAATTTTT--TTTATTTTATGTATATATTTTTTTTTT 15777

Qy        968 AAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGC 1027
              ||       | ||| | |||  |     |  | |   ||   | | |   | | | |
Db      15776 AACATTTTTTTAATTTTTTTTTATTTTATGATATATATTTTTATTTTAATATATTTTTTT 15717

Qy       1028 ATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATAC 1087
               || ||  |||   || |    | |    |||   | |||  | |  ||  ||    |
Db      15716 CTTTTTTTTTTGTTTTTATGATATATATTTTTTTTTTTTTTAATGTTTTTTTTTTTCTTCT 15657

Qy       1088 TTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTT 1147
              ||| ||  || |   || |   |  | |  |||  | |   || |  |   || |||
Db      15656 TTTGTTTTTATTTTTTTTATAATCATTTTTTTTTTTATATAAAATTTTTTTTTAATTTTTT 15597

Qy       1148 TTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGT 1207
              |||       | |  |||||||  |    ||  |||          | ||   |   ||  |
Db      15596 TTTGATAATCTTTTTCATTTTTTATTCTATCAAAATTTATATTTTATTATAATTTTTATT 15537

Qy       1208 AAATGTTAAGAATTTTTTTTATATCTGTT 1236
              |  | |||| || ||||| |   | | ||
Db      15536 ATTTTTTAAAAAATTTTTCTCCTTTTTTT 15508


RESULT 14
US-08-378-313-26
; Sequence 26, Application US/08378313
; Patent No. 6207881
;  GENERAL INFORMATION:
;    APPLICANT:  THEOLOGIS, ATHANASIOS
;    APPLICANT:  SATO, TAKAHIDO
;    TITLE OF INVENTION:  CONTROL OF FRUIT RIPENING THROUGH
;    TITLE OF INVENTION:  GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  MORRISON & FOERSTER
;       STREET:  755 Page Mill Road
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/378,313
;       FILING DATE:
;       CLASSIFICATION:  800
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/862,493
;       FILING DATE:  02-APR-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MURASHIGE, KATE H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  29190-20002.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 856-5600
;       TELEFAX:  (415) 494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7244 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(3056..3226, 3325..3453, 3539..3700, 4582
;       LOCATION:  ..5574)
US-08-378-313-26

  Query Match             4.2%;  Score 52.8;  DB 3;  Length 7244;
  Best Local Similarity   58.1%;  Pred. No. 0.014;
  Matches   93;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy       1092 TTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTC 1151
              || | | | | ||     |||  |||||       |||| | |  | |  ||| | ||
Db       6813 TTTAAACTTAGATAAATCCAAAAGATAATAATTTTGATTGATATTTTATAATGTATCTTT 6872

Qy       1152 TCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAAT 1211
              |  |  ||| |   | |  ||||| |||||    ||  | | ||| || | ||| |||||
Db       6873 TTATCATATTGACATGTAGAAAAATTATAATTTATAATATTTTTTATATAGTTTTTAAAT 6932

Qy       1212 GTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTT 1251
              || | ||||||| ||  |  | ||||| || ||  |||
Db       6933 ATTTAAAATTTTTATTTAAAATATTAAATGAATATATTTT 6972


RESULT 15
US-09-056-075-1/c
; Sequence 1, Application US/09056075
; Patent No. 5955368
;  GENERAL INFORMATION:
;    APPLICANT:  Johnson, Eric A.
;    APPLICANT:  Bradshaw, Marite
;    APPLICANT:  Rood, Julian
;    TITLE OF INVENTION:  Expression System for Clostridium
;    TITLE OF INVENTION:  Species
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,075
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  960296.95238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6243 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  3770..4013
;      OTHER INFORMATION:  /note= "RP4 origin of DNA transfer (oriT) from
;      OTHER INFORMATION:  plasmid RP4"
US-09-056-075-1

  Query Match             4.1%;  Score 52;  DB 2;  Length 6243;
  Best Local Similarity   45.7%;  Pred. No. 0.02;
  Matches  181;  Conservative    0;  Mismatches  215;  Indels    0;  Gaps    0;

Qy        850 TTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGC 909
              || |  ||    ||   |  ||  | |  | ||||     ||  |  | |   |  ||
Db       1488 TTTATAAAGGCTCATTTTTTATATTCTTTTCTTCAAAGATTATATAATATAAAAAAATTT 1429

Qy        910 CTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAA 969
               ||  ||   || | | |||     |||||  ||   ||||| | |  || |  ||
Db       1428 TTTTCAAACTTTAAATAAAAAATATTTTTATATTTTTTTATTTTTTTATTTTTATATTTT 1369

Qy        970 GCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCAT 1029
                 |    |     | ||          | | | || |     | ||||||  || |
Db       1368 TTTATTTTTTATTTTTATATTTTTTTATTTTTATATTTTTTTATTTTTATATTTTTTA 1309

Qy       1030 TATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTT 1089
              | || || ||  || | |       |  ||| | | |||| |||  ||  ||       ||
Db       1308 TTTTTATATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTATTTT 1249

Qy       1090 TCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTT 1149
              | |   |  | |  || | |    | || |||   || || || |  | || | |||
Db       1248 TTTATTTTTTTATTTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTAC 1189

Qy       1150 TCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAA 1209
              ||| |  | |  |  || ||  | |   ||     ||||  |  || |       |
Db       1188 CCTCATTTTTTTACGCTTGTATTATAGGGTACTTTGTACCTGTTCTTTTTTTTGGGGAGG 1129

Qy       1210 ATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAA 1245
              ||| ||||  |||||||  |  ||||  |   ||
Db       1128 TTGTAAAGATAATTTTTTACTTTAGTTAGTTCCGAA 1093


Search completed: August 20, 2003, 15:56:33
Job time : 92 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 13:48:04 ; Search time 309 Seconds
(without alignments)
9145.443 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1257	100.0	1257	10	US-09-938-418-2	Sequence 2, Appli
2	1257	100.0	1257	11	US-09-946-374-430	Sequence 430, App
3	1257	100.0	1257	12	US-10-015-387A-430	Sequence 430, App
4	1257	100.0	1257	12	US-10-063-735-121	Sequence 121, App
5	1257	100.0	1257	12	US-10-006-130A-430	Sequence 430, App
6	1257	100.0	1257	12	US-10-199-672-365	Sequence 365, App
7	1257	100.0	1257	12	US-10-006-172A-430	Sequence 430, App
8	1257	100.0	1257	12	US-10-187-749-365	Sequence 365, App
9	1257	100.0	1257	12	US-10-194-457-365	Sequence 365, App
10	1257	100.0	1257	13	US-10-006-867-121	Sequence 121, App
11	1257	100.0	1257	13	US-10-052-586-365	Sequence 365, App
12	1257	100.0	1257	13	US-10-063-547-121	Sequence 121, App
13	1257	100.0	1257	14	US-10-174-590-365	Sequence 365, App
14	1257	100.0	1257	14	US-10-176-758-365	Sequence 365, App
15	1257	100.0	1257	14	US-10-175-737-365	Sequence 365, App
16	1257	100.0	1257	14	US-10-063-616-121	Sequence 121, App
17	1257	100.0	1257	14	US-10-173-706-365	Sequence 365, App
18	1257	100.0	1257	14	US-10-175-738-365	Sequence 365, App
19	1257	100.0	1257	14	US-10-175-752-365	Sequence 365, App
20	1257	100.0	1257	14	US-10-176-482-365	Sequence 365, App
21	1257	100.0	1257	14	US-10-176-757-365	Sequence 365, App
22	1257	100.0	1257	14	US-10-176-913-365	Sequence 365, App
23	1257	100.0	1257	14	US-10-180-552-365	Sequence 365, App
24	1257	100.0	1257	14	US-10-180-557-365	Sequence 365, App
25	1257	100.0	1257	14	US-10-063-502-121	Sequence 121, App
26	1257	100.0	1257	14	US-10-173-700-365	Sequence 365, App
27	1257	100.0	1257	14	US-10-174-572-365	Sequence 365, App
28	1257	100.0	1257	14	US-10-174-579-365	Sequence 365, App
29	1257	100.0	1257	14	US-10-174-582-365	Sequence 365, App
30	1257	100.0	1257	14	US-10-174-588-365	Sequence 365, App
31	1257	100.0	1257	14	US-10-175-739-365	Sequence 365, App
32	1257	100.0	1257	14	US-10-175-740-365	Sequence 365, App
33	1257	100.0	1257	14	US-10-175-743-365	Sequence 365, App
34	1257	100.0	1257	14	US-10-176-488-365	Sequence 365, App
35	1257	100.0	1257	14	US-10-176-492-365	Sequence 365, App
36	1257	100.0	1257	14	US-10-176-747-365	Sequence 365, App
37	1257	100.0	1257	14	US-10-176-750-365	Sequence 365, App
38	1257	100.0	1257	14	US-10-176-985-365	Sequence 365, App
39	1257	100.0	1257	14	US-10-176-987-365	Sequence 365, App
40	1257	100.0	1257	14	US-10-176-992-365	Sequence 365, App
41	1257	100.0	1257	14	US-10-176-993-365	Sequence 365, App
42	1257	100.0	1257	14	US-10-184-658-365	Sequence 365, App
43	1257	100.0	1257	14	US-10-176-991-365	Sequence 365, App
44	1257	100.0	1257	14	US-10-173-695-365	Sequence 365, App
45	1257	100.0	1257	14	US-10-173-697-365	Sequence 365, App

ALIGNMENTS

RESULT 1
US-09-938-418-2
; Sequence 2, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Gurney,Austin L.
; APPLICANT: Polakis,Paul
; APPLICANT: Williams,P.Mickey
; APPLICANT: Wood,William I.
; APPLICANT: Wu,Thomas D.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18

```
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-938-418-2

  Query Match           100.0%;  Score 1257;  DB 10;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 2
US-09-946-374-430
; Sequence 430, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
```

; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449

```
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match          100.0%;  Score 1257;  DB 11;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 3
US-10-015-387A-430
;  Sequence 430, Application US/10015387A
;  Publication No. US20030135034A1
;  GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT:  Botstein, David
;   APPLICANT:  Desnoyers, Luc
;   APPLICANT:  Eaton, Dan 1.
;   APPLICANT:  Ferrara, Napoleone
;   APPLICANT:  Fong, Sherman
;   APPLICANT:  Gao, Wei-Qiang
;   APPLICANT:  Goddard, Audrey
;   APPLICANT:  Godowski, Paul J.
;   APPLICANT:  Grimaldi, Christopher J.
;   APPLICANT:  Gurney, Austin L.
;   APPLICANT:  Hillan, Kenneth J.
;   APPLICANT:  Pan, James
;   APPLICANT:  Paoni, Nicholas F.
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION:  Acids Encoding the Same
;   FILE REFERENCE: P2830P1C54
;   CURRENT APPLICATION NUMBER: US/10/015,387A
;   CURRENT FILING DATE:  2001-12-12
;   Prior Application removed - See File Wrapper or Palm
;   NUMBER OF SEQ ID NOS: 477
;  SEQ ID NO 430
;    LENGTH: 1257
```

```
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-015-387A-430

  Query Match            100.0%;  Score 1257;  DB 12;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 4
US-10-063-735-121
; Sequence 121, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,735
;  CURRENT FILING DATE:  2002-05-08
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-735-121

  Query Match            100.0%;  Score 1257;  DB 12;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 5
US-10-006-130A-430
; Sequence 430, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-006-130A-430

  Query Match             100.0%;  Score 1257;  DB 12;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
```

```
Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
RESULT 6
US-10-199-672-365
; Sequence 365, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/199,672
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-199-672-365

  Query Match            100.0%;  Score 1257;  DB 12;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
```

```
Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 7
US-10-006-172A-430
; Sequence 430, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 1257; DB 12; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
```

```
Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 8
US-10-187-749-365
; Sequence 365, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-365

Query Match 100.0%; Score 1257; DB 12; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
```

```
Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy      1141 TTTGTTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTTGTTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy      1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 9
US-10-194-457-365
; Sequence 365, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-365

Query Match 100.0%; Score 1257; DB 12; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy        61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy       121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 10
US-10-006-867-121
; Sequence 121, Application US/10006867
; Publication No. US20020119130A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/006,867
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/063435
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/064215
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/083495
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/087759
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/088021
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088029
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088030
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088734
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088740
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088811
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088824
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088825
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088863
;  PRIOR FILING DATE: 1998-06-11
;  PRIOR APPLICATION NUMBER: 60/089105
;  PRIOR FILING DATE: 1998-06-12
;  PRIOR APPLICATION NUMBER: 60/089514
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089653
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089952
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: 60/090246
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090444
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090688
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090696
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090862
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/091628
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/096012
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/096757
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/096949
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/096959
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/097954
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/097971
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/097979
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106030
```

; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/115614
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 1257; DB 13; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 11
US-10-052-586-365
; Sequence 365, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/052,586
;  CURRENT FILING DATE:  2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063564
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063734
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063870
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066120
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/066466
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/069425
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: 60/069870
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/068017
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079664
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/079786
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/080107
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080194
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080327
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/080333
;  PRIOR FILING DATE: 1998-04-01
;  PRIOR APPLICATION NUMBER: 60/081049
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081070
;  PRIOR FILING DATE: 1998-04-08
;  PRIOR APPLICATION NUMBER: 60/081195
;  PRIOR FILING DATE: 1998-04-09
;  PRIOR APPLICATION NUMBER: 60/081838
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082568
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082569
;  PRIOR FILING DATE: 1998-04-21
;  PRIOR APPLICATION NUMBER: 60/082704
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083495
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083496
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083499
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083559
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/084366
;  PRIOR FILING DATE: 1998-05-05
;  PRIOR APPLICATION NUMBER: 60/084414
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/084639
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084640
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084643
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085573
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085580
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085582
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085700
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/086023
```

; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1257; DB 13; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.3e-281;

Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
```

```
Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 12
US-10-063-547-121
; Sequence 121, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,547
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-547-121

  Query Match             100.0%;  Score 1257;  DB 13;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 13
US-10-174-590-365
; Sequence 365, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
```

```
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-174-590-365

  Query Match            100.0%;  Score 1257;  DB 14;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 14
US-10-176-758-365
; Sequence 365, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-176-758-365

  Query Match            100.0%;  Score 1257;  DB 14;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
```

```
Qy       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
RESULT 15
US-10-175-737-365
; Sequence 365, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C50
;  CURRENT APPLICATION NUMBER: US/10/175,737
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-175-737-365

  Query Match            100.0%;  Score 1257;  DB 14;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-281;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
```

```
Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

Search completed: August 20, 2003, 16:01:55
Job time : 314 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 12:28:07 ; Search time 4236 Seconds
(without alignments)
9723.603 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq.old:*
3: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US098D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US099E_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US099F_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US104A_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US104B_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6023A_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6023B_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*
93: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*
94: /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
95: /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*
96: /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*
97: /cgn2_6/ptodata/2/pna/US6042_COMB.seq:*
98: /cgn2_6/ptodata/2/pna/US6043_COMB.seq:*
99: /cgn2_6/ptodata/2/pna/US6044_COMB.seq:*
100: /cgn2_6/ptodata/2/pna/US6045_COMB.seq:*
101: /cgn2_6/ptodata/2/pna/US6046_COMB.seq:*
102: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1257	100.0	1257	39	US-09-938-418-2	Sequence 2, Appli
2	1257	100.0	1257	40	US-09-946-374-430	Sequence 430, App
3	1257	100.0	1257	44	US-10-006-041A-430	Sequence 430, App
4	1257	100.0	1257	44	US-10-006-063A-430	Sequence 430, App

5	1257	100.0	1257	44	US-10-006-116A-430	Sequence 430, App
6	1257	100.0	1257	44	US-10-006-117A-430	Sequence 430, App
7	1257	100.0	1257	44	US-10-006-130A-430	Sequence 430, App
8	1257	100.0	1257	44	US-10-006-172A-430	Sequence 430, App
9	1257	100.0	1257	44	US-10-006-485A-430	Sequence 430, App
10	1257	100.0	1257	44	US-10-006-746A-430	Sequence 430, App
11	1257	100.0	1257	44	US-10-006-768A-430	Sequence 430, App
12	1257	100.0	1257	44	US-10-006-818A-430	Sequence 430, App
13	1257	100.0	1257	44	US-10-006-856A-430	Sequence 430, App
14	1257	100.0	1257	44	US-10-006-867-121	Sequence 121, App
15	1257	100.0	1257	44	US-10-007-194A-430	Sequence 430, App
16	1257	100.0	1257	44	US-10-007-236A-430	Sequence 430, App
17	1257	100.0	1257	44	US-10-011-671A-430	Sequence 430, App
18	1257	100.0	1257	44	US-10-011-692A-430	Sequence 430, App
19	1257	100.0	1257	44	US-10-011-795A-430	Sequence 430, App
20	1257	100.0	1257	44	US-10-011-795B-430	Sequence 430, App
21	1257	100.0	1257	44	US-10-011-833A-430	Sequence 430, App
22	1257	100.0	1257	44	US-10-012-064A-430	Sequence 430, App
23	1257	100.0	1257	44	US-10-012-101B-430	Sequence 430, App
24	1257	100.0	1257	44	US-10-012-121A-430	Sequence 430, App
25	1257	100.0	1257	44	US-10-012-137A-430	Sequence 430, App
26	1257	100.0	1257	44	US-10-012-149A-430	Sequence 430, App
27	1257	100.0	1257	44	US-10-012-231A-430	Sequence 430, App
28	1257	100.0	1257	44	US-10-012-237A-430	Sequence 430, App
29	1257	100.0	1257	44	US-10-012-752A-430	Sequence 430, App
30	1257	100.0	1257	44	US-10-012-753A-430	Sequence 430, App
31	1257	100.0	1257	44	US-10-012-754A-430	Sequence 430, App
32	1257	100.0	1257	44	US-10-012-755A-430	Sequence 430, App
33	1257	100.0	1257	44	US-10-013-430A-430	Sequence 430, App
34	1257	100.0	1257	44	US-10-013-906A-430	Sequence 430, App
35	1257	100.0	1257	44	US-10-013-907A-430	Sequence 430, App
36	1257	100.0	1257	44	US-10-013-909A-430	Sequence 430, App
37	1257	100.0	1257	44	US-10-013-910A-430	Sequence 430, App
38	1257	100.0	1257	44	US-10-013-911A-430	Sequence 430, App
39	1257	100.0	1257	44	US-10-013-912A-430	Sequence 430, App
40	1257	100.0	1257	44	US-10-013-913A-430	Sequence 430, App
41	1257	100.0	1257	44	US-10-013-915A-430	Sequence 430, App
42	1257	100.0	1257	44	US-10-015-385A-430	Sequence 430, App
43	1257	100.0	1257	44	US-10-015-386A-430	Sequence 430, App
44	1257	100.0	1257	44	US-10-015-387A-430	Sequence 430, App
45	1257	100.0	1257	44	US-10-015-388A-430	Sequence 430, App

ALIGNMENTS

```
RESULT 1
US-09-938-418-2
; Sequence 2, Application US/09938418
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Polakis,Paul
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Wu,Thomas D.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF TUMOR
;  FILE REFERENCE: P5009R1
;  CURRENT APPLICATION NUMBER: US/09/938,418
;  CURRENT FILING DATE:  2001-08-23
;  PRIOR APPLICATION NUMBER: 60/081,071
;  PRIOR FILING DATE: 1998-04-07
;  PRIOR APPLICATION NUMBER: 60/085,697
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/097,022
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/101,922
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/103,679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: PCT/US99/05028
;  PRIOR FILING DATE: 1999-03-08
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: PCT/US99/20111
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US00/04342
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-938-418-2

  Query Match           100.0%;  Score 1257;  DB 39;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 2
US-09-946-374-430
; Sequence 430, Application US/09946374
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27

Query Match 100.0%; Score 1257; DB 40; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy      481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy      541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy      601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy      661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy      721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy      781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy      841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy      901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy      961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy     1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy     1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy     1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy     1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 3
US-10-006-041A-430
; Sequence 430, Application US/10006041A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-006-041A-430

Query Match 100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy       61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy      121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy      181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy      241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy      301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy      361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy      421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy      481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy      541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy      601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy      661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy      721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy      781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
```

```
Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 4
US-10-006-063A-430
; Sequence 430, Application US/10006063A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C3
; CURRENT APPLICATION NUMBER: US/10/006,063A
; CURRENT FILING DATE:. 2002-03-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-006-063A-430

Query Match 100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 5
US-10-006-116A-430
; Sequence 430, Application US/10006116A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
```

```
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match           100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 6
US-10-006-117A-430
; Sequence 430, Application US/10006117A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-006-117A-430

  Query Match            100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 7
US-10-006-130A-430
; Sequence 430, Application US/10006130A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C7
```

```
;  CURRENT APPLICATION NUMBER: US/10/006,130A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-006-130A-430

  Query Match             100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 8
US-10-006-172A-430
; Sequence 430, Application US/10006172A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C11
;  CURRENT APPLICATION NUMBER: US/10/006,172A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
```

; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26

```
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match           100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 9
US-10-006-485A-430
; Sequence 430, Application US/10006485A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C9
;  CURRENT APPLICATION NUMBER: US/10/006,485A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
```

; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26

```
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match             100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 10
US-10-006-746A-430
; Sequence 430, Application US/10006746A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C5
;  CURRENT APPLICATION NUMBER: US/10/006,746A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
```

; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26

```
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28
;  PRIOR APPLICATION NUMBER: 60/106029

  Query Match             100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 11
US-10-006-768A-430
; Sequence 430, Application US/10006768A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C10
;  CURRENT APPLICATION NUMBER: US/10/006,768A
;  CURRENT FILING DATE:  2002-03-05
;  NUMBER OF SEQ ID NOS: 477
;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 430
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-006-768A-430

  Query Match             100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
```

```
Qy       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
RESULT 12
US-10-006-818A-430
; Sequence 430, Application US/10006818A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C4
;  CURRENT APPLICATION NUMBER: US/10/006,818A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 430
;   LENGTH: 1257
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-006-818A-430

  Query Match             100.0%;  Score 1257;  DB 44;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-230;
  Matches 1257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

RESULT 13
US-10-006-856A-430
; Sequence 430, Application US/10006856A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 430
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-006-856A-430

Query Match 100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
```

```
Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

```
RESULT 14
US-10-006-867-121
; Sequence 121, Application US/10006867
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/006,867
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/063435
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/064215
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/083495
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/087759
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/088021
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088029
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088030
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: 60/088734
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088740
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088811
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088824
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088825
;  PRIOR FILING DATE: 1998-06-10
;  PRIOR APPLICATION NUMBER: 60/088863
;  PRIOR FILING DATE: 1998-06-11
;  PRIOR APPLICATION NUMBER: 60/089105
;  PRIOR FILING DATE: 1998-06-12
;  PRIOR APPLICATION NUMBER: 60/089514
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089653
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089952
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: 60/090246
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090444
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090688
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090696
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090862
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: 60/091628
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/096012
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/096757
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/096949
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/096959
;  PRIOR FILING DATE: 1998-08-18
;  PRIOR APPLICATION NUMBER: 60/097954
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/097971
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/097979
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/105000
```

; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/112853
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113011
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/115614
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25

Query Match 100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
```

```
Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257


RESULT 15
US-10-007-194A-430
; Sequence 430, Application US/10007194A
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C6
;  CURRENT APPLICATION NUMBER: US/10/007,194A
;  CURRENT FILING DATE:  2002-06-25
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
```

; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882

; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match 100.0%; Score 1257; DB 44; Length 1257;
Best Local Similarity 100.0%; Pred. No. 2.7e-230;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
```

```
Qy       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020

Qy      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080

Qy      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140

Qy      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200

Qy      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
```

Search completed: August 20, 2003, 15:54:54
Job time : 4240 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 13:54:34 ; Search time 210 Seconds
(without alignments)
4507.413 Million cell updates/sec

Title: US-09-938-418-2
Perfect score: 1257
Sequence: 1 ggagagaggcgcgcgggtga.....aataaaaattatttccaaca 1257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 740817 seqs, 376514187 residues

Total number of hits satisfying chosen parameters: 1481634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1253.8	99.7	1284	1	PCT-US02-29560A-5	Sequence 5, Appli
c	2	565.8	45.0	582	6	US-10-470-050-171	Sequence 171, App
	3	435.8	34.7	466	6	US-10-085-783A-57095	Sequence 57095, A
	4	329.8	26.2	395	6	US-10-085-783A-9073	Sequence 9073, Ap
	5	318.4	25.3	396	6	US-10-085-783A-10107	Sequence 10107, A
	6	282.4	22.5	316	6	US-10-085-783A-8707	Sequence 8707, Ap
	7	281.8	22.4	300	6	US-10-085-783A-52366	Sequence 52366, A
	8	267	21.2	555	6	US-10-357-930-45880	Sequence 45880, A
	9	249	19.8	251	6	US-10-085-783A-11744	Sequence 11744, A
c	10	228.8	18.2	1544	6	US-10-357-930-30335	Sequence 30335, A
	11	210.8	16.8	474	6	US-10-357-930-16054	Sequence 16054, A
	12	207.2	16.5	300	6	US-10-085-783A-49278	Sequence 49278, A
	13	196.2	15.6	213	6	US-10-085-783A-52384	Sequence 52384, A
	14	182.4	14.5	398	6	US-10-085-783A-9224	Sequence 9224, Ap
	15	111.6	8.9	139	6	US-10-085-783A-49101	Sequence 49101, A
	16	61.6	4.9	575	6	US-10-626-717-6405	Sequence 6405, Ap
c	17	57.8	4.6	494	6	US-10-357-930-10012	Sequence 10012, A
	18	57	4.5	13831263	5	US-09-947-914-41	Sequence 41, Appl
	19	56.4	4.5	7892	6	US-10-257-166B-138	Sequence 138, App
c	20	56	4.5	15479	6	US-10-257-166B-45	Sequence 45, Appl
	21	55.6	4.4	17848	6	US-10-257-166B-58	Sequence 58, Appl
c	22	54.8	4.4	11422	6	US-10-257-166B-17	Sequence 17, Appl
	23	54.4	4.3	12138	6	US-10-257-166B-115	Sequence 115, App
c	24	53.2	4.2	6002	6	US-10-374-163A-22	Sequence 22, Appl
c	25	52.4	4.2	13831263	5	US-09-947-914-41	Sequence 41, Appl
c	26	52	4.1	50000	5	US-09-662-254B-23	Sequence 23, Appl
c	27	51.4	4.1	591	6	US-10-626-717-6229	Sequence 6229, Ap
	28	51.4	4.1	50000	5	US-09-662-254B-23	Sequence 23, Appl
	29	51	4.1	653	6	US-10-626-717-3404	Sequence 3404, Ap
	30	51	4.1	11422	6	US-10-257-166B-17	Sequence 17, Appl
	31	50.6	4.0	549	6	US-10-621-901-209	Sequence 209, App
	32	50.6	4.0	2475	6	US-10-602-494-305	Sequence 305; App
	33	50.4	4.0	2368	6	US-10-602-494-275	Sequence 275, App
	34	50.2	4.0	5391	6	US-10-257-166B-19	Sequence 19, Appl
	35	50.2	4.0	5909	6	US-10-602-494-142	Sequence 142, App
	36	50.2	4.0	17869	6	US-10-257-166B-1	Sequence 1, Appli
c	37	50	4.0	3505	6	US-10-613-520-204	Sequence 204, App
	38	50	4.0	6106	6	US-10-257-166B-113	Sequence 113, App
	39	50	4.0	8059021	5	US-09-947-914-53	Sequence 53, Appl
	40	49.8	4.0	6216	6	US-10-257-166B-13	Sequence 13, Appl
	41	49.8	4.0	1000000	6	US-10-308-107-2	Sequence 2, Appli
	42	49.6	3.9	8776	6	US-10-257-166B-150	Sequence 150, App
c	43	49.6	3.9	50000	5	US-09-662-254B-24	Sequence 24, Appl
c	44	49.4	3.9	754	7	US-60-480-590-5090	Sequence 5090, Ap
c	45	49.4	3.9	32392	5	US-09-662-254B-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
PCT-US02-29560A-5
; Sequence 5, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560A
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-29560A-5

Query Match 99.7%; Score 1253.8; DB 1; Length 1284;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG 65

Qy         61 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG 125

Qy        121 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG 185

Qy        181 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA 245

Qy        241 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        246 AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT 305

Qy        301 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db        306 GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTC 365

Qy        361 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA 425

Qy        421 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA 485

Qy        481 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA 545

Qy        541 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC 605

Qy        601 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA 665

Qy        661 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT 725

Qy        721 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 785

Qy        781 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC 845

Qy        841 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT 905

Qy        901 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT 965

Qy        961 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA 1025

Qy       1021 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT 1085

Qy       1081 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT 1145

Qy       1141 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC 1205

Qy       1201 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1262
```

RESULT 2
US-10-470-050-171/c
; Sequence 171, Application US/10470050
; GENERAL INFORMATION:
; APPLICANT: Orr, Michael S.
; APPLICANT: Nation, Michele
; APPLICANT: Diggans, James C.
; APPLICANT: Zeng, Wen
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Breast Tissue
; FILE REFERENCE: 44921-5070-US
; CURRENT APPLICATION NUMBER: US/10/470,050
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/263,757
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/286,090
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/292,517
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: PCT/US02/02176
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 1246
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AA584310
US-10-470-050-171

Query Match 45.0%; Score 565.8; DB 6; Length 582;
Best Local Similarity 98.8%; Pred. No. 3.5e-141;
Matches 570; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy        681 AGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGT 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 AGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGT 523

Qy        741 GAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTAC 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 GAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTAC 463

Qy        801 CCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 CCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTA 403

Qy        861 CCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGT 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 CCAAAATAAATGCTTTAATTTTCATTTGCTACCTCGGGTTTTATTATGCCTTGGAATGGT 343

Qy        921 TCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAA 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 TCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAA 283

Qy        981 TATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTG 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 TATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTG 223

Qy       1041 CTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTC 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 CTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTC 163

Qy       1101 ACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTAT 1160
              |||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||
Db        162 ACATTCTCTCAACCTATGAGGGGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTAT 103

Qy       1161 AGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAAT 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 AGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAAT 43

Qy       1221 TTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              |||||||||||||||||||||||||||||||||||||
Db          42 TTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 6
```

RESULT 3
US-10-085-783A-57095
; Sequence 57095, Application US/10085783A

```
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57095
;   LENGTH: 466
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)..(19)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (457)..(457)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-57095

  Query Match             34.7%;  Score 435.8;  DB 6;  Length 466;
  Best Local Similarity   98.9%;  Pred. No. 1.7e-106;
  Matches  448;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy        693 AATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGT 752
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 AATTCNACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGT 73

Qy        753 GCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGAT 812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGAT 133

Qy        813 GCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACC-AAAATAAAT 871
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        134 GCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAAATAAAT 193

Qy        872 GCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATG 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATG 253

Qy        932 ACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAG 991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAG 313

Qy        992 ACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAA 1051
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 ACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAA 373

Qy       1052 AGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCA 1111
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGTGGTTTCAACATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCA 433

Qy       1112 ACCTATAATTTGGAATATTGTTGTGGTCTTTTG 1144
              |||||||||||||||||||||| || ||||||
Db        434 ACCTATAATTTGGAATATTGTTGNGGGCTTTTG 466


RESULT 4
US-10-085-783A-9073
; Sequence 9073, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9073
;   LENGTH: 395
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-9073

  Query Match             26.2%;  Score 329.8;  DB 6;  Length 395;
  Best Local Similarity   99.4%;  Pred. No. 3.3e-78;
  Matches  331;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        649 CCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATA 708
              | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGAGTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATA 122

Qy        709 TTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATG 182

Qy        769 TTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGA 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 TTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGA 242

Qy        829 ATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTG 302

Qy        889 CTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTT 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTT 362

Qy        949 ATGTATACATCTGAATGAAAAGCAAAGCTAAAT 981
              |||||||||||||||||||||||||||||||||
Db        363 ATGTATACATCTGAATGAAAAGCAAAGCTAAAT 395


RESULT 5
US-10-085-783A-10107
; Sequence 10107, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10107
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (23)..(23)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
```

```
;   NAME/KEY: misc_feature
;   LOCATION: (27)..(29)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (75)..(75)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (147)..(147)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (150)..(150)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (210)..(210)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (222)..(222)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (251)..(251)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (262)..(262)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (305)..(305)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (351)..(351)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (382)..(382)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-10107

  Query Match            25.3%;  Score 318.4;  DB 6;  Length 396;
  Best Local Similarity  96.7%;  Pred. No. 3.7e-75;
  Matches  319;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        597 TGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAA 656
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGTCAGCGNTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAA 126

Qy        657 GCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGC 716
              |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Db        127 GCTATAATTTATTTGGACCANGGNAGCCCTGAAATGAATTCAACAATTAATATTCATCGC 186

Qy        717 ACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATC 776
              |||||||||||||||||||||| |||||||||| ||||||||| ||||||||||||||
Db        187 ACTTCTTCTGTGGAAGGACTTTGNGAAGGAATTGGNGCTGGATTAGCGGATGTTGCTATC 246

Qy        777 TGGGTTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTT 836
              |||| |||||||||| ||||||||||||||||||||||||||||||||||||||||| |
Db        247 TGGGNTGGCACTTGTNCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGNT 306

Qy        837 TCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCT 896
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        307 TCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTNTCATTTGCTACCTCT 366

Qy        897 TTTTTTATTATGCCTTGGAATGGTTCACTT 926
              |||||||||||||| ||||||||||||||
Db        367 TTTTTTATTATGCCTNGGAATGGTTCACTT 396
```

```
RESULT 6
US-10-085-783A-8707
; Sequence 8707, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8707
;   LENGTH: 316
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (53)..(53)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (196)..(196)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (259)..(259)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (268)..(268)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-8707

  Query Match            22.5%;  Score 282.4;  DB 6;  Length 316;
  Best Local Similarity  95.8%;  Pred. No. 1.3e-65;
  Matches  298;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    1;

Qy        949 ATGTATACATCTGAATGAAAAGCA--AAGCTAAATATGTTTACAGACCAAAGTGTGATTT 1006
              |||||||||||||||| |||||||| |      |||||||||||||||||||| |||||||
Db          1 ATGTATACATCTGAANGAAAAGCAAGAGCTAGAATATGTTTACAGACCAAAGNGTGATTT 60

Qy       1007 CACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATT 1066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATT 120

Qy       1067 TTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAA 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAA 180

Qy       1127 TATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCT 1186
              ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 TATTGGTGTGGTCTTNTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCT 240

Qy       1187 ACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTTATATCTGTTAAATAAAAAT 1246
              |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db        241 ACCAATCTTTGTACAATTNGTAAATGTNAAGAATTTTTTTTTATATCTGTTAAATAAAAAT 300

Qy       1247 TATTTCCAACA 1257
              ||||||||||| 
Db        301 TATTTCCAACA 311
```

```
RESULT 7
US-10-085-783A-52366
; Sequence 52366, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52366
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (56)..(56)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (179)..(179)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (183)..(183)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (274)..(274)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (296)..(296)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-52366

  Query Match           22.4%;  Score 281.8;  DB 6;  Length 300;
  Best Local Similarity   95.7%;  Pred. No. 1.9e-65;
  Matches  286;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy        952 TATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACAC 1011
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||
Db          2 TATACATNTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTNCACAC 61

Qy       1012 TGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTT 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTT 121

Qy       1072 TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTG 1131
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        122 TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATANTG 181

Qy       1132 TTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAA 1191
              | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TNGTGGGCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAA 241

Qy       1192 TCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATT 1250
              |||||||||||||||||||||||||||||||| |||||||||| ||  ||||    ||
Db        242 TCTTTGTACAATTTGTAAATGTTAAGAATTTTNTTTATATCTGTAAATAAAAATNATTT 300


RESULT 8
US-10-357-930-45880
; Sequence 45880, Application US/10357930
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45880
;   LENGTH: 555
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-357-930-45880

  Query Match           21.2%;  Score 267;  DB 6;  Length 555;
  Best Local Similarity   98.2%;  Pred. No. 2.6e-61;
  Matches  270;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        506 TGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 565
              | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 TCCAGGATGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 340

Qy        566 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 400

Qy        626 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCC 460

Qy        686 TGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGG 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 TGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGG 520

Qy        746 AATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG 780
              |||||||||||||||| ||||||||||||||||||
Db        521 AATTGGTGCTGGATTAATGGATGTTGCTATCTGGG 555


RESULT 9
US-10-085-783A-11744
; Sequence 11744, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
```

```
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11744
;   LENGTH: 251
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (130)..(130)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(133)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-11744

  Query Match             19.8%;  Score 249;  DB 6;  Length 251;
  Best Local Similarity   99.2%;  Pred. No. 9.6e-57;
  Matches  249;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1003 ATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAA 1062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAA 60

Qy       1063 TATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTT 1122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTT 120

Qy       1123 GGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAA 1182
             ||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATATTGNTGNGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAA 180

Qy       1183 AGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAA 1242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAA 240

Qy       1243 AAATTATTTCC 1253
             ||||||||||||
Db        241 AAATTATTTCC 251


RESULT 10
US-10-357-930-30335/c
; Sequence 30335, Application US/10357930
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30335
;   LENGTH: 1544
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1531, 1544
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-30335

  Query Match             18.2%;  Score 228.8;  DB 6;  Length 1544;
  Best Local Similarity   96.5%;  Pred. No. 8.6e-51;
  Matches  245;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    1;

Qy        506 TGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 565
              | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TCCAGGATGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 438

Qy        566 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 378

Qy        626 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 AGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCC 318

Qy        686 TGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGA--AGGACTTTGTGAA 743
              |||||||||||||||||||||||||||||||||||||||||||  ||||||| |||||
Db        317 TGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGACCAGGACTTGGTGAA 258

Qy        744 GGAATTGGTGCTGG 757
              ||||| ||||| ||
Db        257 GGAATCGGTGCCGG 244


RESULT 11
US-10-357-930-16054
; Sequence 16054, Application US/10357930
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16054
;   LENGTH: 474
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 305, 432
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-16054

  Query Match             16.8%;  Score 210.8;  DB 6;  Length 474;
  Best Local Similarity   95.6%;  Pred. No. 2.4e-46;
  Matches  237;  Conservative    0;  Mismatches    9;  Indels    2;  Gaps    2;

Qy        506 TGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 565
              | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 TCCAGGATGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGG 284

Qy        566 CTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 625
              ||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        285 CTCACTTTGGCTAAAATGCANAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGG 344

Qy        626 AGC-TGAATGTTCAGGACCTCTTCCCA-TTGAAGCTATAATTTATTTGGACCAAGGAAGC 683
              ||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        345 AGCTTGAATGTTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAGC 404

Qy        684 CCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAA 743
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        405 CCTGAAATGAATTCAACAATTAATATTNATCGCACTTCTTCTGTGGAAGGACTTTGTGAA 464

Qy        744 GGAATTGG 751
                |||||
Db        465 AGAATTTG 472


RESULT 12
US-10-085-783A-49278
; Sequence 49278, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49278
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (46)..(46)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (53)..(53)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143)..(143)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)..(152)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (157)..(157)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (209)..(209)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (221)..(221)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (245)..(245)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (263)..(263)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (274)..(274)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (287)..(287)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-49278

  Query Match             16.5%;  Score 207.2;  DB 6;  Length 300;
  Best Local Similarity   87.2%;  Pred. No. 1.6e-45;
  Matches  266;  Conservative    0;  Mismatches   34;  Indels    5;  Gaps    4;

Qy        794 AGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGA 853
              ||||||||||||||||||||||||||||||||||||||||||| ||| ||   |      | |
Db          1 AGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATACAGGTTTNTGGCATNATTATTG 60

Qy        854 AGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTG 913
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         61 AAGACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTGG 120

Qy        914 GAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAA 973
              |||||| |||||||||||||| ||||||||  |||| ||||||||||||||||||||||
Db        121 GAATGG-TCACTTAAATGACATTNTAAATAAG-NTATGNATACATCTGAATGAAAAGCAA 178

Qy        974 AGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAAATCTAGCATTATT 1033
              |||||||||||| |||||||||||||||||| ||||||||| || ||||||||||||||||
Db        179 AGCTAAATATGGTTACAGACCAAAGTGTGANTTCACACTG-TTNTAAATCTAGCATTATT 237

Qy       1034 CATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTT 1093
              ||||||| |||||||||||| || | |||||  ||||| ||  || ||| | ||||||||
Db        238 CATTTTGNTTCAATCAAAAGGGGGTNCAATA--TTTTTNAGGGGGGTAGGANACTTTCTT 295

Qy       1094 CATAG 1098
              |||||
Db        296 CATAG 300


RESULT 13
US-10-085-783A-52384
; Sequence 52384, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 52384
;   LENGTH: 213
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (30)..(30)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (32)..(32)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (37)..(37)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (41)..(41)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (111)..(111)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119)..(119)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (128)..(129)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (138)..(138)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (168)..(168)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (175)..(175)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (197)..(197)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-52384

  Query Match             15.6%;  Score 196.2;  DB 6;  Length 213;
  Best Local Similarity   93.0%;  Pred. No. 1.1e-42;
  Matches  198;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1040 GCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGT 1099
             ||||||||||||||||||||||||||||| | |||| ||  ||||||||||||||||||
Db          1 GCTTCAATCAAAAGTGGTTTCAATATTTTNTNTAGTNGGCNAGAATACTTTCTTCATAGT 60

Qy       1100 CACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTA 1159
             |||||||||||||||||||||||||||||||||||||||||||| |||| ||||||| |
Db         61 CACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGGTTTTNCTCTTAGNA 120

Qy       1160 TAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAA 1219
             |||||||  |||||||| |||||||||||||||||||||||||||| |||||  |||||
Db         121 TAGCATTNNTAAAAAAANATAAAAGCTACCAATCTTTGTACAATTTGNAAATGCNAAGAA 180

Qy       1220 TTTTTTTTATATCTGTTAAATAAAAATTATTTC 1252
             ||||||||||||||| ||||||||||||||||
Db        181 TTTTTTTTATATCTGTNAAATAAAAATTATTTC 213


RESULT 14
US-10-085-783A-9224
```

```
; Sequence 9224, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9224
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (165)..(165)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (207)..(207)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (218)..(218)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (259)..(259)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (295)..(295)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (307)..(307)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (345)..(345)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (398)..(398)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-9224

  Query Match             14.5%;  Score 182.4;  DB 6;  Length 398;
  Best Local Similarity   85.9%;  Pred. No. 8.5e-39;
  Matches  281;  Conservative    0;  Mismatches   33;  Indels   13;  Gaps    7;

Qy        323 GCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCT-GGGATCCCAG 381
              ||||||||||||||||||||||||||||||  ||||||||||||||| |||||||||
Db         66 GCCTGGTCGAGACGGGAGCCCTGGGGCCAATGGCATTCCGGGTACACCTGGGGATCCCAG 125

Qy        382 GTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT 441
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        126 GTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGANGGAAAGCTTTGAGGAGTCCT 185

Qy        442 GGACA-CCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGG 500
              |||||  |||||||||||||| |||||||||  ||||||||||||||||||||||||||||
Db        186 GGACACCCCAACTACAAGCAGNGTTCATGGAGNTCATTGAATTATGGCATAGATCTTGGG 245

Qy        501 -AAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGA----GTTT 555
               |||||||||||| ||||||||||||||||||| |  ||    |  ||   |     |||
Db        246 AAAAATTGCGGAGNGTACATTTACAAAGATGCGGTTCAAATAAGTGCTCNTAAGAGTTTT 305
```

```
Qy        556 TGTTCAGTGGCTCAC-TTCGGCTAAAATGCAGAAATGCATGCTGTCAGC----GTTGGTA 610
              ||||||||||||||| |||||||||||||||||||  |       |   |    |||||||
Db        306 GNTTCAGTGGCTCACTTTCGGCTAAAATGCAGAAAATCCNTGCCTGGCCAGCGGTTGGTA 365

Qy        611 TTTCAC-ATTCAATGGAGCTGAATGTT 636
              |||||| |||||||||||||||||| |
Db        366 TTTCACAATTCAATGGAGCTGAATGGT 392


RESULT 15
US-10-085-783A-49101
; Sequence 49101, Application US/10085783A
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49101
;   LENGTH: 139
;   TYPE: DNA
;   ORGANISM: Human
US-10-085-783A-49101

  Query Match             8.9%;  Score 111.6;  DB 6;  Length 139;
  Best Local Similarity   96.6%;  Pred. No. 3.4e-20;
  Matches  114;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1140 TTTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTA 1199
              |||  ||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db          8 TTTGATTTTTGCTCTTAGTATAGCATTGTTAAAAAAATATAAAAGCTACCAATCTTTGTA 67

Qy       1200 CAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA 125


Search completed: August 20, 2003, 16:05:41
Job time : 220 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 13, 2003, 13:15:11 ; Search time 84 Seconds
(without alignments)
459.173 Million cell updates/sec

Title: US-09-938-418-7
Perfect score: 1301
Sequence: 1 MRPQGPAASPQRLRGLLLLL.....GDASTGWNSVSRIIIEELPK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	243	21	AAY99441	Human PRO1755 (UNQ
2	1301	100.0	243	21	AAY99462	Human PRO1550 amin
3	1301	100.0	243	22	AAU29206	Human PRO polypept
4	1301	100.0	243	22	AAB87586	Human PRO1550. Ho
5	1301	100.0	243	22	AAB66190	Protein of the inv
6	1301	100.0	243	22	AAB66211	Protein of the inv
7	1301	100.0	243	23	ABP68636	Human pancreatic c
8	1301	100.0	243	23	ABG95911	Human secreted/tra
9	1301	100.0	243	23	ABG78938	Human breast tumou
10	1301	100.0	243	23	ABB95545	Human angiogenesis
11	1301	100.0	243	23	AAE20462	Human tumour-assoc
12	1301	100.0	243	23	ABB84939	Human PRO1550 prot
13	1301	100.0	243	24	ABU71294	Human PRO1550 prot
14	1301	100.0	243	24	ABU71566	Human secreted pol
15	1301	100.0	243	24	ABU72012	Novel human secret
16	1301	100.0	243	24	ABU72169	Human PRO polypept
17	1301	100.0	243	24	ABU65751	Human secreted/tra
18	1301	100.0	243	24	ABU66084	Novel human secret
19	1301	100.0	243	24	ABU67588	Human secreted/tra
20	1301	100.0	243	24	ABG75948	Human antigenic ta
21	1301	100.0	243	24	ABU65446	Human PRO polypept
22	1301	100.0	243	24	ABJ37761	Human tumour-relat
23	1301	100.0	243	24	ABU58582	Human PRO polypept
24	1301	100.0	243	24	ABU56118	Human secreted/tra
25	1301	100.0	243	24	ABU57113	Human PRO polypept
26	1301	100.0	243	24	ABU10692	Human secreted/tra
27	1301	100.0	278	23	ABP68637	Human pancreatic c
28	1301	100.0	278	23	ABG78939	Human breast tumou
29	1301	100.0	278	24	ABJ37762	Human tumour-relat
30	1294	99.5	243	22	AAB36667	Human secretory pr
31	1294	99.5	243	23	ABG96340	Human ovarian canc
32	1294	99.5	243	23	ABJ05554	Breast cancer-asso
33	1294	99.5	243	23	ABB80978	Human REMODELIN po
34	1294	99.5	243	24	ABR48227	Human bladder canc
35	1294	99.5	243	24	ABG75758	Human REMODELIN pr
36	1294	99.5	243	24	ABU56607	Lung cancer-associ
37	1294	99.5	278	21	AAB08856	Amino acid sequenc
38	1294	99.5	278	22	AAM25746	Human protein sequ
39	1294	99.5	278	23	ABG96338	Human ovarian canc
40	1294	99.5	278	24	ABR47627	Breast cancer asso
41	1291	99.2	243	21	AAY91529	Human secreted pro
42	1291	99.2	278	23	ABP68631	Human pancreatic c
43	1289	99.1	243	24	ABJ37031	Human breast cance
44	1216	93.5	245	23	ABB80977	Rat REMODELIN poly
45	1216	93.5	245	24	ABG75757	Rat REMODELIN prot

ALIGNMENTS

RESULT 1
AAY99441
ID AAY99441 standard; Protein; 243 AA.
XX
AC AAY99441;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1755 (UNQ828) amino acid sequence SEQ ID NO:352.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.

PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR N-PSDB; AAA37123.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 12; Fig 204; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.3e-122;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 2
AAY99462
ID AAY99462 standard; Protein; 243 AA.
XX
AC AAY99462;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1550 amino acid sequence SEQ ID NO:431.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.

```
PR   17-NOV-1998;   98US-0108801.
PR   17-NOV-1998;   98US-0108802.
PR   17-NOV-1998;   98US-0108806.
PR   17-NOV-1998;   98US-0108807.
PR   17-NOV-1998;   98US-0108867.
PR   17-NOV-1998;   98US-0108925.
PR   18-NOV-1998;   98US-0108848.
PR   18-NOV-1998;   98US-0108849.
PR   18-NOV-1998;   98US-0108850.
PR   18-NOV-1998;   98US-0108851.
PR   18-NOV-1998;   98US-0108852.
PR   18-NOV-1998;   98US-0108858.
PR   18-NOV-1998;   98US-0108904.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   N-PSDB; AAA37144.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or
PT   secreted PRO polypeptides, useful for screening of potential peptide or
PT   small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS   Claim 12; Fig 246; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC   PCR primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 21;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 3
AAU29206
ID   AAU29206 standard; Protein; 243 AA.
XX
AC   AAU29206;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Human PRO polypeptide sequence #183.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46107.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 11; Fig 366; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
```

```
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence   243 AA;

  Query Match           100.0%;  Score 1301;  DB 22;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 4
AAB87586
ID   AAB87586 standard; Protein; 243 AA.
XX
AC   AAB87586;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1550.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92118.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping. -
XX
PS   Claim 12; Fig 122; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping.
XX
SQ   Sequence   243 AA;

  Query Match           100.0%;  Score 1301;  DB 22;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 5
AAB66190
ID   AAB66190 standard; protein; 243 AA.
XX
AC   AAB66190;
XX
DT   02-APR-2001  (first entry)
XX
DE   Protein of the invention #102.
XX
KW   Secreted; transmembrane; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US04342.
XX
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
```

```
PR   01-SEP-1999;   99WO-US20111.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy -
XX
PS   Claim 1; Fig 204; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of
CC   anti-sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents.
CC   The nucleic acids may also be used in gene therapy.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 1301;  DB 22;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 6
AAB66211
ID   AAB66211 standard; protein; 243 AA.
XX
AC   AAB66211;
XX
DT   02-APR-2001  (first entry)
XX
DE   Protein of the invention #123.
XX
KW   Secreted; transmembrane; gene therapy.
XX
OS   Unidentified.
XX
PN   WO200078961-A1.
XX
PD   28-DEC-2000.
XX
PF   18-FEB-2000; 2000WO-US04342.
XX
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   01-SEP-1999;   99WO-US20111.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-071395/08.
XX
PT   Secreted and transmembrane proteins and nucleic acids designated PRO,
PT   useful as hybridization probes, in chromosome and gene mapping and gene
PT   therapy -
XX
PS   Claim 1; Fig 246; 787pp; English.
XX
CC   The present invention relates to secreted and transmembrane proteins.
CC   These proteins and the DNA encoding them may be used as hybridization
CC   probes, in chromosome and gene mapping and in the generation of
CC   anti-sense RNA and DNA. They may also be used used to generate either
CC   transgenic animals or knockout animals which are in turn useful for
CC   development and screening of therapeutically useful reagents.
CC   The nucleic acids may also be used in gene therapy.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 1301;  DB 22;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 7
ABP68636
ID   ABP68636 standard; Protein; 243 AA.
XX
AC   ABP68636;
XX
DT   14-JAN-2003  (first entry)
```

XX
DE Human pancreatic cancer expressed protein SEQ ID NO 4559.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US02781.
XX
PR 30-JAN-2001; 2001US-265305P.
PR 31-JAN-2001; 2001US-265682P.
PR 09-FEB-2001; 2001US-267568P.
PR 21-MAR-2001; 2001US-278651P.
PR 28-APR-2001; 2001US-287112P.
PR 16-MAY-2001; 2001US-291631P.
PR 12-JUL-2001; 2001US-305484P.
PR 20-AUG-2001; 2001US-313999P.
PR 27-NOV-2001; 2001US-333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
DR N-PSDB; ABV99144.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
PT for diagnosing, preventing and/or treating cancer, particularly
PT pancreatic cancer -
XX
PS Claim 2; SEQ ID NO 4559; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC (b) complements of (a); (c) sequences consisting of at least 20
CC contiguous residues of (a); (d) sequences that hybridize to (a), under
CC moderately stringent conditions; (e) sequences having at least 75% or 90%
CC identity to (a); or (f) degenerate variants of (a). Polypeptides
CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
CC detect cancer in a patient and compositions comprising polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations and
CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The
CC polynucleotides can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 23; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.3e-122;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

RESULT 8
ABG95911
ID ABG95911 standard; Protein; 243 AA.
XX
AC ABG95911;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1550.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-0006867.
XX
PR 29-OCT-1997; 97US-063435P.
PR 29-OCT-1997; 97US-064215P.
PR 22-APR-1998; 98US-082797P.
PR 29-APR-1998; 98US-083495P.
PR 15-MAY-1998; 98US-085579P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 11-JUN-1998; 98US-088863P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089514P.
PR 16-SEP-1998; 98WO-US19330.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21194.
PR 22-DEC-1999; 99WO-US30720.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32378.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2002-731348/79.
DR N-PSDB; ABS74438.

```
XX
PT   New isolated secreted and transmembrane PRO polypeptide useful for
PT   modulating biological activity of a cell, or for treating
PT   sports-related joint problems, osteoarthritis or rheumatoid arthritis
XX
PS   Claim 20; Fig 122; 399pp; English.
XX
CC   The invention relates to an isolated secreted and transmembrane PRO
CC   polypeptide having 80 % sequence identity to a sequence appearing
CC   as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
CC   an extracellular domain of the proteins with their associated signal
CC   peptide or lacking its associated signal peptide. Also included are
CC   the nucleic acids encoding the proteins, vectors, host cells,
CC   fusion proteins and antibodies which specifically bind to the proteins.
CC   The proteins are useful for detecting a polypeptide designated as A, B, C
CC   or D in a sample suspected of containing an A, B, C or D polypeptide,
CC   by contacting the sample with a polypeptide designated as E, F, G, H or
CC   I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
CC   or D/I polypeptide conjugate in the sample, where the formation of the
CC   conjugate is indicative of the presence of an A, B, C or D polypeptide
CC   in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
CC   polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
CC   E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
CC   polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
CC   polypeptide. The sample comprises a cell suspected of expressing the A,
CC   B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
CC   a detectable label or is attached to a solid support. The proteins are
CC   useful for linking a bioactive molecule to a cell expressing a
CC   polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
CC   molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
CC   causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
CC   against them are useful for modulating a biological activity of a cell
CC   expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
CC   I. The cell is killed. The proteins are useful for identifying
CC   agonists or antagonists, for the preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the proteins, as
CC   molecular weight markers for protein electrophoresis purposes, and as
CC   therapeutic agents for treating sports-related joint problems,
CC   articular cartilage defects, osteoarthritis or rheumatoid arthritis.
CC   Nucleic acids encoding the proteins are useful as hybridisation probes,
CC   in chromosome and gene mapping, in the generation of anti-sense RNA and
CC   DNA, for the preparation of the proteins, to generate transgenic or
CC   knockout animals which are useful in the development and screening of
CC   therapeutic useful reagents, for chromosome identification, and in gene
CC   therapy. The antibody is useful as a therapeutic agent, in a diagnostic
CC   assay and for affinity purification of the protein from recombinant
CC   cell culture natural sources. The present sequence represents a novel
CC   secreted or transmembrane protein of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 9
ABG78938
ID   ABG78938 standard; Protein; 243 AA.
XX
AC   ABG78938;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human breast tumour polypeptide #29.
XX
KW   Human; breast tumour protein; breast cancer; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2002085998-A1.
XX
PD   04-JUL-2002.
XX
PF   13-APR-2001; 2001US-0834759.
XX
PR   28-DEC-1998;   98US-0222575.
PR   02-APR-1999;   99US-0285480.
PR   23-JUN-1999;   99US-0339338.
PR   02-SEP-1999;   99US-0389681.
PR   03-NOV-1999;   99US-0433826.
PR   17-APR-2000; 2000US-0551621.
PR   08-JUN-2000; 2000US-0590751.
PR   22-JUN-2000; 2000US-0604287.
PR   20-JUL-2000; 2000US-0620405.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Jiang Y,  Dillon DC,  Mitcham JL,  Xu J,  Harlocker SL,  Hepler WT;
PI   Henderson RA;
XX
DR   WPI; 2002-635657/68.
DR   N-PSDB; ABS64028, ABS64029.
XX
PT   Novel breast cancer polynucleotides and polypeptides encoded by the
PT   polynucleotides, useful for detecting the presence of breast cancer in
PT   a patient, and in pharmaceutical compositions, for treating breast
PT   cancer -
XX
PS   Claim 2; Page 235-236; 247pp; English.
XX
CC   The invention relates to an isolated breast tumour polynucleotide and the
CC   polypeptide it encodes. The polynucleotide and polypeptide are useful for
CC   detecting the presence of breast cancer in a patient, and in
CC   pharmaceutical compositions for treating breast cancer. The sequences are
CC   useful for stimulating an immune response in a patient and can therefore
CC   be used in production of vaccines. The sequences are also useful for
CC   detecting the presence of a cancer in a patient, by obtaining a
CC   biological sample from the patient, contacting the biological sample with
CC   a composition of the invention and detecting the amount of polynucleotide
CC   that hybridizes to the sample. This sequence represents a human breast
CC   tumour polypeptide of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
```

```
Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 10
ABB95545
ID   ABB95545 standard; Protein; 243 AA.
XX
AC   ABB95545;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human angiogenesis related protein PRO1550 SEQ ID NO: 246.
XX
KW   Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW   atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW   cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW   antiarteriosclerotic.
XX
OS   Homo sapiens.
XX
PN   WO200208284-A2.
XX
PD   31-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-US21735.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   15-SEP-2000; 2000US-000000P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   28-JUN-2001; 2001WO-US00000.
XX
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-171999/22.
DR   N-PSDB; ABL95683.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 11; Fig 246; 567pp; English.
XX
CC   The present invention provides the protein and coding sequences of human
CC   PRO proteins. These are useful for treating or diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder, including cardiac
CC   hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The present sequence is a PRO protein of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 11
AAE20462
ID   AAE20462 standard; Protein; 243 AA.
XX
AC   AAE20462;
```

```
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human tumour-associated antigenic target-170 (TAT170) protein.
XX
KW   Human; tumour-associated antigenic target-170; TAT170; cytostatic;
KW   gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Signal_peptide
FT   Protein         31..243
FT                   /label= Mature_TAT170_protein
FT   Modified-site   67..72
FT                   /note= "N-myristoylation site"
FT   Modified-site   117..122
FT                   /note= "N-myristoylation site"
FT   Modified-site   163..168
FT                   /note= "N-myristoylation site"
FT   Modified-site   186..189
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   199..204
FT                   /note= "N-myristoylation site"
FT   Modified-site   203..208
FT                   /note= "N-myristoylation site"
XX
PN   WO200216602-A2.
XX
PD   28-FEB-2002.
XX
PF   23-AUG-2001; 2001WO-US26626.
XX
PR   24-AUG-2000; 2000WO-US23328.
PR   01-DEC-2000; 2000WO-US32678.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Goddard A,  Godowski PJ,  Gurney AL,  Polakis P;
PI   Williams PM,  Wood WI,  Wu TD,  Zhang Z;
XX
DR   WPI; 2002-292065/33.
DR   N-PSDB; AAD32717.
XX
PT   New antibodies that bind tumor-associated antigenic target (TAT)
PT   polypeptides, useful for treating and diagnosing tumor (e.g. breast,
PT   lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
PT   pigs, goats, rabbits or humans
XX
PS   Claim 1; Fig 7; 124pp; English.
XX
CC   The present invention relates to an isolated antibody that binds to
CC   tumor-associated antigenic target (TAT) polypeptide. The antibody is
CC   used for treating and diagnosing tumours (e.g. breast, lung, liver or
CC   stomach tumours) in mammals, e.g. dogs, cats, cattle, horses, sheep,
CC   pigs, goats, rabbits, or preferably humans. The antibody may also be
CC   used in antibody-dependent enzyme mediated prodrug therapy (ADEPT).
CC   The antibody is also useful for the therapeutic treatment or for the
CC   diagnostic detection of cancer. TAT cDNA is useful in gene therapy.
CC   The present sequence is human TAT170 protein. TAT170 cDNA is designated
CC   as DNA76393-1664.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
    Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 12
ABB84939
ID   ABB84939 standard; Protein; 243 AA.
XX
AC   ABB84939;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO1550 protein sequence SEQ ID NO:246.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US19692.
XX
PR   23-JUN-2000; 2000US-213637P.
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
```

```
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI   Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR   WPI; 2002-090516/12.
DR   N-PSDB; ABL88194.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 11; Fig 246; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence   243 AA;

  Query Match            100.0%;  Score 1301;  DB 23;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 13
ABU71294
ID   ABU71294 standard; Protein; 243 AA.
XX
AC   ABU71294;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Human PRO1550 protein.
XX
KW   Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW   tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW   differentiation; tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003036143-A1.
XX
PD   20-FEB-2003.
XX
PF   02-JUL-2002; 2002US-0187600.
XX
PR   16-SEP-1998;   98WO-US19330.
PR   07-OCT-1998;   98WO-US21141.
PR   01-DEC-1998;   98WO-US25108.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28551.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   28-JUL-2000; 2000WO-US20710.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   20-JUN-2001; 2001WO-US19692.
PR   29-JUN-2001; 2001WO-US21066.
PR   09-JUL-2001; 2001WO-US21735.
PR   29-AUG-2001; 2001WO-US27099.
PR   18-SEP-1997;   97US-059263P.
PR   18-SEP-1997;   97US-059266P.
PR   17-OCT-1997;   97US-062250P.
PR   21-OCT-1997;   97US-063486P.
PR   24-OCT-1997;   97US-063120P.
PR   24-OCT-1997;   97US-063121P.
PR   28-OCT-1997;   97US-063540P.
PR   28-OCT-1997;   97US-063541P.
PR   28-OCT-1997;   97US-063544P.
PR   28-OCT-1997;   97US-063564P.
PR   29-OCT-1997;   97US-063734P.
PR   31-OCT-1997;   97US-063870P.
PR   31-OCT-1997;   97US-064103P.
PR   13-NOV-1997;   97US-065311P.
PR   21-NOV-1997;   97US-066120P.
PR   24-NOV-1997;   97US-066466P.
PR   24-NOV-1997;   97US-066772P.
PR   11-DEC-1997;   97US-069335P.
PR   12-DEC-1997;   97US-069425P.
```

PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.
PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 1301; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.3e-122;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
Db 1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy 61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
Db 61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy 121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
Db 121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
Db 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

```
Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 14
ABU71566
ID   ABU71566 standard; Protein; 243 AA.
XX
AC   ABU71566;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Human secreted polypeptide PRO1550.
XX
KW   Human; gene therapy; tumour; cancer.
XX
OS   Homo sapiens.
XX
PN   US2003013855-A1.
XX
PD   16-JAN-2003.
XX
PF   03-MAY-2002; 2002US-0063616.
XX
PR   30-DEC-1998;   98KR-0062142.
PR   08-MAR-1999;   99WO-US05028.
PR   14-MAY-1999;   99WO-US10733.
PR   30-DEC-1999;   99WO-US31274.
PR   18-FEB-2000; 2000WO-US04341.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   21-MAR-2000; 2000WO-US07532.
PR   22-MAY-2000; 2000WO-US14042.
PR   02-JUN-2000; 2000WO-US15264.
PR   24-AUG-2000; 2000WO-US23328.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-JUN-2001; 2001WO-US17800.
PR   14-MAY-1999;   99US-0311832.
PR   25-AUG-1999;   99US-0380137.
PR   25-AUG-1999;   99US-0380138.
PR   25-AUG-1999;   99US-0380139.
PR   25-AUG-1999;   99US-0380142.
PR   15-SEP-1999;   99US-0397342.
PR   18-OCT-1999;   99US-0403297.
PR   12-NOV-1999;   99US-0423844.
PR   22-AUG-2000; 2000US-0644848.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   08-NOV-2000; 2000US-0709238.
PR   20-DEC-2000; 2000US-0747259.
PR   22-MAR-2001; 2001US-0816744.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   30-MAY-2001; 2001US-0870574.
PR   05-JUN-2001; 2001US-0874503.
PR   29-JUN-2001; 2001US-0869599.
PR   18-JUL-2001; 2001US-0908827.
PR   06-DEC-2001; 2001US-0006867.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-330485/31.
DR   N-PSDB; ACA58870.
XX
PT   New isolated antibody specifically binding a PRO polypeptide, useful
PT   for the preparation of a medicament for treating disorders with the
PT   aberrant expression or activity of the PRO polypeptide, such as tumor
PT   conditions and cancer  -
XX
PS   Disclosure; Page 194-195; 406pp; English.
XX
CC   The invention relates to an antibody that binds to a polypeptide with a
CC   fully defined sequence given in the specification. The methods and
CC   compositions (containing antibodies that specifically bind a PRO
CC   polypeptide) of the present invention are useful for the preparation of a
CC   medicament for the treatment of disorders associated with the aberrant
CC   expression or activity of the PRO polypeptide, such as tumour conditions
CC   and cancer. They can also be used to generate transgenic or knockout
CC   animals useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC   molecular weight markers for protein electrophoresis, chromosome
CC   identification and tissue typing. The PRO polypeptides are useful to
CC   induce angiogenesis e.g wound healing; in the treatment of sports-related
CC   joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC   arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC   antibodies may be used in various diagnostic, competitive binding and/or
CC   immunoprecipitation assays. The present sequence represents the amino
CC   acid sequence of a PRO polypeptide of the invention.
XX
SQ   Sequence   243 AA;

  Query Match             100.0%;  Score 1301;  DB 24;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-122;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243


RESULT 15
ABU72012
ID   ABU72012 standard; Protein; 243 AA.
XX
AC   ABU72012;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO1550.
XX
KW   Human; secreted and transmembrane polypeptide;
KW   chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW   therapeutic agent screening; chromosome identification; tissue typing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003018183-A1.
XX
PD   23-JAN-2003.
XX
PF   01-MAY-2002; 2002US-0063512.
```

XX
PR 06-DEC-2001; 2001US-0006867.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330984/31.
DR N-PSDB; ACA60423.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody -
XX
PS Disclosure; Fig 122; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO poypeptide.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1301; DB 24; Length 243;
Best Local Similarity 100.0%; Pred. No. 8.3e-122;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60

Qy         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120

Qy        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180

Qy        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240

Qy        241 LPK 243
              |||
Db        241 LPK 243
```

Search completed: August 13, 2003, 13:25:07
Job time : 86 secs